

58662
Delaval, Jan

From: Jamroz, Margaret
Sent: Tuesday, January 22, 2002 8:12 AM
To: Delaval, Jan
Subject: 09/628,126

Jan,

Please do open search SEQ ID NOS: 6, 8, 19, and 23 with interference for 09/628,126.

Thanks,
Margaret (Megan) Jamroz
USPTO
AU 1644
Mailbox 9E12
CM1 9D04
(703) 308-8365

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

Access DB# 58662

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
Art Unit: _____ Phone Number 30 _____ Serial Number: _____
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4488
jan.delaval@uspto.gov

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: <u>C. Jan</u>	NA Sequence (#) _____	STN _____
Searcher Phone #: <u>1446</u>	AA Sequence (#) <u>4</u>	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>1/22</u>	Bibliographic _____	Dr. Link _____
Date Completed: <u>1/22</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/>
Clerical Prep Time: <u>10</u>	Patent Family _____	WWW/Internet _____
Online Time: <u>10</u>	Other _____	Other (specify) _____

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 22, 2002, 08:16:15 ; Search time 78.06 Seconds
(without alignments)
226.794 Million cell updates/sec

Title: US-09-628-126-6
Perfect score: 1246
Sequence: 1 MEFCLQAGSCGAPSPDPAM.....DTNFTPLDNLVSLYSSD 239

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Maximum Match 0%
Listing first 45 summaries

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22: /SID52/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	1246	100.0	239 14 AAR45008	Sequence encoded b
2	1141	91.6	220 14 AAR45006	Sequence encoded b
3	860.5	69.1	234 14 AAR45009	Sequence encoded b
4	814.5	65.4	215 14 AAR45007	Sequence encoded b
5	742	59.6	21 AAB08277	Amino acid sequenc
6	600	48.2	143 21 AAB08276	Amino acid sequenc
7	126	10.1	279 17 AAR88357	Mouse Fas ligand.
8	123	9.9	279 16 AAR79098	Mouse Fas ligand.
9	110	8.8	279 16 AAR77282	Mouse Fas-L protei
10	109	8.7	179 16 AAR79069	Mouse Fas ligand (
11	102	8.2	278 16 AAR79095	Rat Fas ligand enc

12	102	8.2	278	20	AAR98069	Rat Fas ligand (Fa
13	102	8.2	278	20	AAR95040	Rat FasL protein.
14	97	7.8	138	16	AAR79068	Mouse Fas ligand (
15	97	7.8	143	21	AA080266	Amino acid sequenc
16	96	7.7	281	22	AA040556	Human Fas ligand p
17	95.5	7.7	258	20	AA040371	Human Fas ligand d
18	95	7.6	137	16	AAR79067	Mouse Fas ligand (
19	92	7.4	271	20	AA028596	Fas ligand (FasL)
20	91	7.3	179	16	AAR79066	Rat Fas ligand (pa
21	91	7.3	309	16	AAR64189	Murine 4-1BB-L pol
22	91	7.3	309	18	AA026656	Murine 4-1BB ligand
23	89.5	7.2	268	19	AA048953	Non-cleavable Fas
24	88.5	7.1	448	21	AA028694	PC-muAGP-1 (99-291
25	88	7.1	281	20	AA040373	Human Fas ligand d
26	88	7.1	281	21	AA087576	Human Fas ligand (
27	88	7.1	281	21	AA087581	Human Fas ligand (
28	87	7.0	265	19	AA048954	Non-cleavable Fas
29	87	7.0	277	20	AA040372	Human Fas ligand d
30	87	7.0	281	16	AAR77281	Human Fas-L protei
31	87	7.0	281	16	AAR79097	Human Fas ligand.
32	87	7.0	281	17	AAR98104	Human Fas ligand d
33	87	7.0	281	17	AAR88356	Human Fas ligand.
34	87	7.0	281	18	AA027143	Human Fas ligand.
35	87	7.0	281	19	AA075959	Human Fas ligand.
36	87	7.0	281	19	AA049105	Fas ligand. Mamma
37	87	7.0	281	20	AA028594	Wild type Fas liga
38	87	7.0	281	20	AA098071	Human Fas ligand (
39	87	7.0	281	20	AA095041	Human FasL protein
40	87	7.0	281	21	AA019342	Amino acid sequenc
41	87	7.0	281	21	AA087569	Human Fas ligand (
42	87	7.0	281	21	AA087577	Human Fas ligand (
43	87	7.0	281	21	AA087578	Human Fas ligand (
44	87	7.0	281	21	AA087579	Human Fas ligand (
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ALIGNMENTS

RESULT 1
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ID AAR45008 standard; Protein; 239 AA.
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AC AAR45008;
XX
DT 19-JUN-1994 (first entry)
XX
DE Sequence encoded by a murine CD30-L cDNA clone
DE encoding additional N-terminal amino acids.
XX
KW Hodgkin's disease; lymphoma; surface antigen; cytokine;
KW CD30 ligand; CD30-L; TNF; NGF.
XX

OS Acomys cahirinus.
XX
XX key Location/Qualifiers
FH Region 47..67
FT /label= Transmembrane
FT
XX
PN WO9324135-A.
XX
PD 09-DEC-1993.
XX
XX 25-MAY-1993; 93WO-US04926.
XX
XX 26-MAY-1992; 92US-0889717.
PR 02-JUN-1992; 92US-0892459.
PR 15-JUN-1992; 92US-0899660.
PR 01-JUL-1992; 92US-0907224.
PR 27-OCT-1992; 92US-0966775.
XX
PA (IMMV) IMMUNEX CORP.
XX

PI Armitage RJ, Goodwin RG, Smith CA;
 XX WPI: 1993-405417/50.
 DR N-PSDB; AAQ53537.
 XX
 PT New cytokine, CD30-L, which binds CD30 - used for developing
 PT prods. for diagnosis, detection, purifications, research and
 PT therapy
 XX
 PS Claim 15; Figure 6a; 59pp; English.
 XX
 CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
 CC as a clinical marker for Hodgkin's lymphoma and related haematologic
 CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
 CC L and other derived prods. can be used for elucidating the roles
 CC that CD30 and CD30-L may play in the immune system and for diagnosis
 CC and therapy. It can be isolated as follows. A cDNA library prepd. from
 CC the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion
 CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L
 CC (AAQ53535). This cDNA can then be used as a probe to screen a human PBL
 CC cDNA library to obtain cDNA encoding human CD30-L (AAQ53536). An
 CC anchored PCR technique was employed to isolate CD30-L human and murine
 CC clones containing an additional 19 N-terminal amino acid sequence
 CC (AAQ53537, AAQ53538).
 XX
 SQ Sequence 239 AA;
 Query Match 100.0%; Score 1246; DB 14; Length 239;
 Best Local Similarity 100.0%; Pred. No. 1.8e-116;
 Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEPLQAGSCGAPSPDAMQVPGSVASPRWRSTRPWRSTRSYFYLSLTALVCLVAVVA 60
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 QY 121 NEDGTIHLIYQDGNLIVQPGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKKQTLVT 180
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 ID AAR45006
 XX AAR45006 standard; Protein; 220 AA.
 AC AAR45006;
 XX
 DT 19-JUN-1994 (first entry)
 XX
 DE Sequence encoded by a murine CD30-L cDNA clone.
 XX
 KW Hodgkin's disease; lymphoma; surface antigen; cytokine;
 KW CD30 ligand; CD30-L; TNF; NGF.
 XX
 OS Acomys cahirinus.
 XX
 XX Key Location/Qualifiers
 FT Region 28..48
 FT /label= transmembrane
 XX
 XX WO9324135-A.
 XX
 XX Q9-DEC-1993.
 PD
 XX 25-MAY-1993; 93WO-US04926.
 PF

XX 26-MAY-1992; 92US-0889717.
 PR 02-JUN-1992; 92US-0892459.
 PR 15-JUN-1992; 92US-0899660.
 PR 01-JUL-1992; 92US-0907224.
 PR 27-OCT-1992; 92US-0966775.
 XX (IMV) IMMUNEX CORP.
 XX
 PI Armitage RJ, Goodwin RG, Smith CA;
 XX
 XX WPI: 1993-405417/50.
 DR N-PSDB; AAQ53535.
 XX
 PT New cytokine, CD30-L, which binds CD30 - used for developing
 PT prods. for diagnosis, detection, purifications, research and
 PT therapy
 XX
 PS Claim 15; Figure 3a; 59pp; English.
 XX
 CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
 CC as a clinical marker for Hodgkin's lymphoma and related haematologic
 CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
 CC L and other derived prods. can be used for elucidating the roles
 CC that CD30 and CD30-L may play in the immune system and for diagnosis
 CC and therapy. It can be isolated as follows. A cDNA library prepd. from
 CC the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion
 CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L.
 CC This cDNA can then be used as a probe to screen a human PBL cDNA
 CC library to obtain cDNA encoding human CD30-L.
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 Query Match 91.6%; Score 1141; DB 14; Length 220;
 Best Local Similarity 100.0%; Pred. No. 5e-106;
 Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 QY 80 APLKGGNCSEDLFCTLKSTPSKKSWAYLQVSKHLNNTKLSWNEDEGTIHLIYQDGNLIVQ 139
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 ID AAR45009
 XX AAR45009 standard; Protein; 234 AA.
 AC AAR45009;
 XX
 DT 19-JUN-1994 (first entry)
 XX
 DE Sequence encoded by a human CD30-L cDNA clone
 DE encoding additional N-terminal amino acids.
 XX
 KW Hodgkin's disease; lymphoma; surface antigen; cytokine;
 KW CD30 ligand; CD30-L; TNF; NGF.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Region 41..62

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OM protein - protein search, using sw model

Run on: January 22, 2002, 08:21:17 ; Search time 78.06 Seconds
(without alignments)
208.764 Million cell updates/sec

Title: US-09-628-126-19
Perfect score: 1141
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Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /SID52/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1141	100.0	220	14	AA1980
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3	814.5	71.4	215	14	AA1982
4	814.5	71.4	234	14	AA1983
5	742	65.0	143	21	AA1984
6	600	52.6	143	21	AA1985
7	112	9.8	279	17	AA1986
8	109	9.6	179	16	AA1987
9	109	9.6	279	16	AA1988
10	104	9.1	279	16	AA1989
11	97	8.5	138	16	AA1990

12	97	8.5	143	21	AA1980	Amino acid sequenc
13	95	8.3	137	16	AA1981	Mouse Fas ligand (
14	93	8.2	281	22	AA1982	Human Fas ligand p
15	92.5	8.1	258	20	AA1983	Human Fas ligand d
16	91	8.0	179	16	AA1984	Rat Fas ligand (pa
17	91	8.0	278	16	AA1985	Rat Fas ligand enc
18	91	8.0	278	20	AA1986	Rat Fas ligand (Fa
19	91	8.0	278	20	AA1987	Rat FasL protein.
20	89	7.8	271	20	AA1988	Fas ligand (FasL)
21	88.5	7.8	309	16	AA1989	Murine 4-1BB-L pol
22	88.5	7.8	309	18	AA1990	Murine 4-1BB ligand
23	88.5	7.8	448	21	AA1991	FC-muAGP-1 (99-291
24	87	7.6	2013	21	AA1992	Plasmodium falcipa
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26	86	7.5	319	22	AA1994	Human T2R44 amino
27	85	7.4	143	21	AA1995	Amino acid sequenc
28	85	7.4	281	20	AA1996	Human Fas ligand d
29	85	7.4	281	21	AA1997	Human Fas ligand (
30	85	7.4	281	21	AA1998	Human Fas ligand (
31	85	7.4	291	18	AA1999	Mouse apoptosis in
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33	85	7.4	291	19	AA2001	Murine AGP-1. Mus
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ALIGNMENTS

RESULT 1
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ID AA1980 standard; Protein; 220 AA.
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AC AA1980;
XX
DT 19-JUN-1994 (first entry)
XX
DE Sequence encoded by a murine CD30-L cDNA clone.
DE
KW Hodgkin's disease; lymphoma; surface antigen; cytokine;
KW CD30 ligand; CD30-L; TNF; NGF.
XX
OS Acomys cahirinus.
XX
XX
FH Key Location/Qualifiers
FT Region 28..48
FT /label= transmembrane
XX
PN WO9324135-A.
XX
PD 09-DEC-1993.
XX
PF 25-MAY-1993; 93WO-US04926.
XX
PR 26-MAY-1992; 92US-0889717.
PR 02-JUN-1992; 92US-0892459.
PR 15-JUN-1992; 92US-0899660.
PR 01-JUL-1992; 92US-0907224.
PR 27-OCT-1992; 92US-0966775.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Armitage RJ, Goodwin RG, Smith CA;


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XX PN WO93241135-A.
XX PD
XX PP
XX PF
XX PR
XX PR
XX PR
XX PR
XX PR
XX PA (IMMV ) IMMUNEX CORP.
XX PA Armitage RJ, Goodwin RG, Smith CA;
XX PI WPI; 1993-405417/50.
XX DR N-PSDB; AAQ53536.
XX PT
XX PS New cytokine, CD30-L, which binds CD30 - used for developing
    prods. for diagnosis, detection, purifications, research and
    therapy
    Claim 15; Figure 5a; 59pp; English.
XX CC
XX CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
    as a clinical marker for Hodgkin's lymphoma and related haematologic
    malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
    L and other derived prods. can be used for elucidating the roles
    that CD30 and CD30-L may play in the immune system and for diagnosis
    and therapy. It can be isolated as follows. A cDNA library prepd. from
    the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion
    protein labelled with (125)I to obtain cDNA encoding murine CD30-L.
    This cDNA can then be used as a probe to screen a human PBL cDNA
    library to obtain cDNA encoding human CD30-L.
XX SQ Sequence 215 AA;
    Query Match 71.4%; Score 814.5; DB 14; Length 215;
    Best Local Similarity 70.6%; Pred. No. 5e-75;
    Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps
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1 mhvpagsvas-----hlgtarsyflttatlaiclvftvatimvlvvgqrdspnpsd 54
QY 60 KAPLKGNCSEDLFCFLTKSTPSKKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLI 119
55 nvpikggnccsedllcilkrpfkkswaylqvakhlnktklwnkdgilhgvr yqgnlvi 114
QY 120 QFGELFEIVCQLQFLVCNSHNHSDVLTQLLLINSIKKQTLVTVCESGVOSKNIIYQNLSOF 179
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
115 qfbglyflicqlfvlqcpgnsavdlklellinkhkikqalvtvcsgmqtckhv ygalsgf 174
QY 180 LLHYLVQNVSTISVRVDNFQYVDNTPEPLDNVLSRVLYSSDD 220
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
175 lldylqvnttisivnvdtffydttstiplenvisiflynsnd 215
RESULT 4
AAR45009
ID AAR45009 standard; Protein; 234 AA.
XX AC AAR45009;
XX DT
XX DT 19-JUN-1994 (first entry)
XX DE
DE DE Sequence encoded by a human CD30-L cDNA clone
XX DE encoding additional N-terminal amino acids.
XX KW Hodgkin's disease; lymphoma; surface antigen; cytokine;

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KW		CD30 ligand; CD30-L; TNF; NGF.
XX		Homo sapiens.
OS		Key Location/Qualifiers
FH		Region 41..62
FT		/label= Transmembrane
FT		
XX		W09324135-A.
PN		09-DEC-1993.
PD		
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PF		
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PR		02-JUN-1992; 92US-0892459.
PR		15-JUN-1992; 92US-0899660.
PR		01-JUL-1992; 92US-0907224.
PR		27-OCT-1992; 92US-0966775.
XX		(IMMV) IMMUNEX CORP.
PA		
XX		Armitage RJ, Goodwin RG, Smith CA;
PI		
XX		WPI; 1993-405417/50.
DR		N-PSDB; AAQ53538.
DR		
XX		New cytokine, CD30-L, which binds CD30 - used for developing
PT		prots., for diagnosis, detection, purifications, research and
PT		therapy
PT		
XX		Claim 15; Figure 7a; 59pp; English.
XX		
CC		CD30-L is a ligand for CD30, the 120kd surface antigen widely used
CC		as a clinical marker for Hodgkin's lymphoma and related haematologic
CC		malignancies. CD30 is a member of the TNF/MGF superfamily. The CD30-
CC		L and other derived prods. can be used for elucidating the roles
CC		that CD30 and CD30-L may play in the immune system and for diagnosis
CC		and therapy. It can be isolated as follows. A cDNA library prepd.from
CC		the murine helper T-cell line 7B9 is screened with a CD30/FC fusion
CC		protein labelled with (125)I to obtain cDNA encoding murine CD30-L
CC		(AAQ53535). This cDNA can then be used as a probe to screen a human PBL
CC		cDNA library to obtain cDNA encoding human CD30-L (AAQ53536). An
CC		anchored PCR technique was employed to isolate CD30-L human and murine
CC		clones containing an additional 19 N-terminal amino acid sequence
CC		(AAQ53537, AAQ53538).
XX		
SQ		Sequence 234 AA;
		Query Match 71.4%; Score 814.5; DB 14; Length 234;
		Best Local Similarity 70.6%; Pred. No. 5.6e-75;
		Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps
Qy	1	MQVPGSVASPWRSRTPRWSTSRSYFYLLSTAL-VCLVVAVAILLVVVKRKDSTPNTE 59 : : :
Db	20	mhhvpgsvas-----hlgtetsrsyflltatlalclvtvatimlvvrqtdsi pnsqd 73 : : :
Qy	60	KAPLKGNCSEDLFLCTLKSTSPKSKSWAYLOVSKHLNTKLWNEDGTHGLYQDGNLIV 119 : :
Db	74	nvpklgncsedliliclkrapfkkswaylqvakhlnkktklswnkdgillhgvyqdgnlvi 133 : :
Qy	120	QFPGLYFTVCOLQELVOCNSHSVDLTQLLLNSKIKKOTLTVTCESGVQSKNINYLNLSOF 179 : :
Db	134	qfpglyftlicqlqfvqpccnssvdkieellinkhkikkalvtccesgmqtkhvyqnlsqf 193 : :
Qy	180	LLHYLQVNSTISVRDNFYVDTFNFPLDNVLVSPLYSSSD 220 : :
Db	194	lldylqvnstisrvndtfpydtstffplenvlsiflysnsd 234 : :
RESULT	5	
AAB08277		

ID AAB08277 standard; Protein; 143 AA.
 AC AAB08277;
 XX 04-DEC-2000 (first entry)
 XX Amino acid sequence of a mouse TNF ligand CD30L.
 DE AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;
 XX type II transmembrane protein; B cell stimulatory factor;
 KW inflammatory disorder; immune disorder; rheumatoid arthritis;
 KW lupus and graft versus host disease.
 XX Homo sapiens.
 OS Mus sp.
 XX WO200047740-A2.
 PN 17-AUG-2000.
 XX 11-FEB-2000; 2000WO-US03653.
 PF 12-FEB-1999; 99US-0119906.
 XX 18-NOV-1999; 99US-0166271.
 PR (AMGE-) AMGEN INC.
 XX Boyle WJ, Hsu H;
 PI WPI; 2000-558217/51.
 XX Novel polypeptides comprising tumour necrosis factor ligand family
 PT proteins, useful for treating inflammatory and immune disorders, e.g.
 PT rheumatoid arthritis -
 XX Claim 14; Fig 9; 7lpp; English.
 XX AAB08265-83 represent tumour necrosis factor (TNF) ligands. The
 CC specification describes an AGP-3 polypeptide, which is TNF ligand
 CC family member. AGP-3 is a type II transmembrane protein, and is a
 CC potent B cell stimulatory factor. Expression of AGP-3 correlates to
 CC increases in the number of B cells and immunoglobulins produced.
 CC AGP-3 proteins, antibodies, and nucleic acids may be used to treat
 CC inflammatory and immune disorders, e.g. rheumatoid arthritis,
 CC Crohn's disease, lupus and graft versus host disease. The nucleic
 CC acids may be used to regulate the expression of an AGP-3 related
 CC protein. The AGP-3 proteins, antibodies and nucleic acids are also
 CC useful for the detection of AGP-3 agonists, antagonists and
 CC characterizing interactions with AGP-3 related proteins.
 XX Sequence 143 AA;
 SQ
 Query Match 55.0%; Score 742; DB 21; Length 143;
 Best Local Similarity 100.0%; Pred. No. 7e-68;
 Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 78 STPSKSWAYLOYSKHLNNTKLSWNEDGTHGLIYQDGNLIVQPPGLYFTVCQLQFLVQC 137
 Db 1 stpskswaylvqskhlntklswnedgthgliyqdgndlvqppgllyftvcqlqflvqc 60
 QY 138 SNHSDVLTQLLINSKIKKOTLVTVCSGVQSKNIYQNLQSLFLHYLQVNSTISVRVDF 197
 Db 61 snhsdvltqllinskkkqtlvtvcesgvqskniyqnlqslflhyqvntisvrdf 120
 QY 198 QYVDTNFTPLDNVLSVFLYSSSD 220
 Db 121 qyvdtntfpldnvlsvflysssd 143
 RESULT 6
 AAB08276
 ID AAB08276 standard; Protein; 143 AA.
 XX

AC AAB08276;
 XX 04-DEC-2000 (first entry)
 XX Amino acid sequence of a human TNF ligand CD30L.
 DE AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;
 KW type II transmembrane protein; B cell stimulatory factor;
 KW inflammatory disorder; immune disorder; rheumatoid arthritis;
 KW lupus and graft versus host disease.
 XX Homo sapiens.
 OS WO200047740-A2.
 PN 17-AUG-2000.
 XX 11-FEB-2000; 2000WO-US03653.
 PF 12-FEB-1999; 99US-0119906.
 XX 18-NOV-1999; 99US-0166271.
 PR (AMGE-) AMGEN INC.
 XX Boyle WJ, Hsu H;
 PI WPI; 2000-558217/51.
 XX Novel polypeptides comprising tumour necrosis factor ligand family
 PT proteins, useful for treating inflammatory and immune disorders, e.g.
 PT rheumatoid arthritis -
 XX Claim 14; Fig 9; 7lpp; English.
 XX AAB08265-83 represent tumour necrosis factor (TNF) ligands. The
 CC specification describes an AGP-3 polypeptide, which is TNF ligand
 CC family member. AGP-3 is a type II transmembrane protein, and is a
 CC potent B cell stimulatory factor. Expression of AGP-3 correlates to
 CC increases in the number of B cells and immunoglobulins produced.
 CC AGP-3 proteins, antibodies, and nucleic acids may be used to treat
 CC inflammatory and immune disorders, e.g. rheumatoid arthritis,
 CC Crohn's disease, lupus and graft versus host disease. The nucleic
 CC acids may be used to regulate the expression of an AGP-3 related
 CC protein. The AGP-3 proteins, antibodies and nucleic acids are also
 CC useful for the detection of AGP-3 agonists, antagonists and
 CC characterizing interactions with AGP-3 related proteins.
 XX Sequence 143 AA;
 SQ
 Query Match 52.6%; Score 600; DB 21; Length 143;
 Best Local Similarity 77.3%; Pred. No. 2.1e-53;
 Matches 109; Conservative 19; Mismatches 13; Indels 0; Gaps 0;
 QY 80 PSKSWAYLOYSKHLNNTKLSWNEDGTHGLIYQDGNLIVQPPGLYFTVCQLQFLVQC 139
 Db 3 pfkkswaylvqskhlntklswnedgthgliyqdgndlvqppgllyftvcqlqflvqc 62
 QY 140 HSDVLTQLLINSKIKKOTLVTVCSGVQSKNIYQNLQSLFLHYLQVNSTISVRVDF 199
 Db 63 nsdvltqllinskkkqtlvtvcesgvqskniyqnlqslflhyqvntisvrdf 122
 QY 200 VDTNFTPLDNVLSVFLYSSSD 220
 Db 123 idtstfpldnvlsflysssd 143
 RESULT 7
 AAB08357
 ID AAB08357 standard; Protein; 279 AA.
 XX
 AC AAB08357;
 XX


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PF 10-NOV-1994; 94WO-JF01899.
XX
PR 18-OCT-1994; 94JP-0278378.
PR 10-NOV-1993; 93JP-0305975.
PR 13-DEC-1993; 93JP-0342526.
PR 18-MAR-1994; 94JP-0074344.
PR 08-JUL-1994; 94JP-0180955.
PR 07-SEP-1994; 94JP-0239363.
XX
PA (NOCH ) MOCHIDA PHARM CO LTD.
PA (OSAB-) OSAKA BIOSCIENCE INST.
XX
XX Nagata S, Nakamura N, Suda T, Takahashi T;
XX WPI; 1995-194031/25.
DR N-PSDB; AAQ99496.
XX
XX Peptide which binds to Fas antigen, and antibody reactive with it
XX for treatment and diagnosis of viral or auto-immune diseases
XX
XX Claim 9; Page 219-221; 300pp; Japanese.
XX
XX Fas ligands or active fragments able to induce apoptosis in cells
XX which express the Fas cell surface antigen are claimed. The
XX proteins are isolated from human, rat and mouse sources. The present
XX sequence represents part of the mouse Fas ligand.
XX
XX Sequence 137 AA;
SQ
Query Match 8.3%; Score 95; DB 16; Length 137;
Best Local Similarity 24.4%; Pred. No. 0.057;
Matches 32; Conservative 27; Mismatches 46; Indels 26; Gaps 6;
OY 84 SWAYLVQSKHLNNTKLSWNED-GT--IHGLIYQDGNLIVQPGGLYFIVCOLOFLVQ-CSN 139
Db 1 svahltgnphrsipewedytgailsrgvxykkggvinetgylfvyyskvyfrgqscnn 60
OY 140 HSYVDLTLQLLNSK-----IKKQTLVTVCESG-----VQSKNIYQNLQSQ 178
Db 61 qpinkhkvymr-nskypedlvmeekrlnycttgqiwahssylgaavfalsadhylyvnisq 119
OY 179 FLHYLYQVNST 189
Db 120 lslnfeeskt 130
RESULT 14
AAU04556
ID AAU04556 standard; Protein; 281 AA.
XX
XX AAU04556;
XX
XX 26-SEP-2001 (first entry)
XX
XX Human Fas ligand protein, FasL.
XX
XX Human; FasL; tumour necrosis factor; apoptosis; cancer; tumour;
XX hepatocellular carcinoma.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 120 /note= "Encoded by CAG"
XX Misc-difference 227 /note= "Encoded by GGC"
XX Misc-difference 265 /note= "Encoded by CCT"
XX
XX Wo200151503-A1.
XX
XX 19-JUL-2001.
XX
PD

```

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XX 04-JAN-2001; 2001WO-US00529.
XX
XX 07-JAN-2000; 2000US-0479524.
XX
XX (BIOC-) BIOCRYSTAL LTD.
XX
XX Barbera-Guillem E;
XX
XX WPI; 2001-442131/47.
XX N-PSDB; AAS08454.
XX
XX New polynucleotides comprising Fas ligand sense, Fas ligand antisense
XX polynucleotides or their combinations, for inhibiting solid nonlymphoid
XX tumour progression in an individual.
XX
XX Example 1; Page 37-39; 43pp; English.
XX
XX The sequence is the Human Fas ligand, FasL, a type II transmembrane
XX protein of the tumour necrosis factor family. Fas mediated apoptosis
XX requires cross-linking with FasL. FasL polynucleotides, antisense FasL
XX polynucleotides and their combinations are used in the manufacture of a
XX pharmaceutical composition for inhibiting tumour progression in an
XX individual, by administering the composition intratumorally into the
XX solid tumour of the individual. Types of tumours and cancers
XX include hepatocellular carcinoma and non-lymphoid tumours of the brain,
XX liver, lung, lymph node, bone marrow, breast, colon, pancreas, stomach,
XX prostate, or reproductive tract.
XX
XX Sequence 281 AA;
SQ
Query Match 8.2%; Score 93; DB 22; Length 281;
Best Local Similarity 21.3%; Pred. No. 0.24;
Matches 44; Conservative 37; Mismatches 62; Indels 64; Gaps 10;
OY 34 VCLVVAVAIILVLV-----QKKDSTPN--TTEKAPLKGKNCSEDLFC 74
Db 81 lc1lvmfmvalvglgmfglqhlqkelaelrestnmhtasslekgihps----- 135
OY 75 TLKSTPSKSW---AYLVQSKHLNNTKLSWNEDGTI---HGLIYQDGNLIVQPGGLYFIV 128
Db 136 ---pppekkelrkvhltgksnsrsmplewedtygivilsgvxykkggvinetgylfvy 192
OY 129 COLOFLVQ-CSN-----HSVDLTLQLLNSK-----IKKQTLVTVCESG----- 166
Db 193 skvyfrgqscnnlplshkv-----ymrnskyppqdlvmmeeknmnsycttgqmwarsylga 247
OY 167 ----VQSKNIYQNLQSQFLHYLYQVNST 189
Db 248 vfnltsadhylyvnselslvnfeesqt 274
RESULT 15
AAU04371
ID AAU04371 standard; Protein; 258 AA.
XX
XX AAU04371;
XX
XX 24-JUN-1999 (first entry)
XX
XX Human Fas ligand derivative #1.
XX
XX Human; Fas ligand derivative; antagonist; apoptosis modulator;
XX apoptosis inducer; cytotoxic activity; protease resistant; cancer;
XX viral infection; autoimmune disease; gene therapy.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO9914325-A1.
XX
XX 25-MAR-1999.
XX
PD

```



```
XX 17-SEP-1998; 98WO-JP04187.
XX
XX 17-SEP-1997; 97JP-0252541.
XX
XX (MOCH ) MOCHIDA PHARM CO LTD.
XX PA (OSAB-) OSAKA BIOSCIENCE INST.
XX
XX PI Nagata S, Tanaka M;
XX
XX WPI; 1999-229531/19.
XX DR N-PSDB; AAX33116.
XX
XX PT Protease-resistant Fas ligand derivatives used for prevention of,
XX e.g. cancer
XX
XX PS Claim 4; Page 46-47; 60pp; Japanese.
XX
XX CC The present sequence is a protease-resistant Fas ligand derivative
XX in which a region of human Fas ligand which is susceptible to protease
XX attack has been deleted. The present invention also describes apoptosis
XX modulators containing soluble Fas ligand. The modification in the Fas
XX ligand renders it resistant to the action of proteases such as the
XX metalloproteinase which in vivo cleaves the active membrane-bound Fas
XX ligand (which is active as an apoptosis inducer). The Fas ligand can be
XX used for the prevention and treatment of diseases such as cancer, viral
XX infection and autoimmune disease, e.g. by introduction of DNA encoding
XX the modified Fas ligand into effector cells using a suitable gene
XX therapy vector.
XX
XX SQ Sequence 258 AA;

Query Match      8.1%; Score 92.5; DB 20; Length 258;
Best Local Similarity 21.0%; Pred. No. 0.24; Mismatches 53; Indels 73; Gaps 9;
Matches 42; Conservative 32;

QY 34 VCLVAVAILVLV-----QKSDTPNTERKAPLKGNGCSEDLFCTLKSTPS 81
Db 81 lcclvmfmvlgvalgigmgfqlhqlkepspp-----pe 116
QY 82 KKS-----AYLQVSKHLNNTKLSWNEDGTI---HGLIYQGNLIVQPGLYFIVCQLQFLV 135
Db 117 kkelrkvahltgksnsrsmplewedtygivilsgvkkkgivinetglyfyvyskvyfgr 176
QY 136 Q-CSN---HSVDLTLLQLINSK-----IKKQTLVTVCESG-----VQS 169
Db 177 qscnplplshkv-----ymrnskyppqdlvmmegkmmusycttdgqmwarsyylgavfntsa 231
QY 170 KNIYQNLQFLHLYLQVNST 189
Db 232 dhlyvnselsivnfeesqt 251
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Search completed: January 22, 2002, 08:21:18
Job time: 303 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 22, 2002, 08:21:17 ; Search time 78.06 Seconds
(without alignments)
222.049 Million cell updates/sec

Title: US-09-628-126-8
Perfect score: 1220
Sequence: 1 MDPGLQALNGMAPPDGTAM.....DTSTFPLENLSIFLYNSD 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_1101.*

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1: /SIDS2/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseq/AA1985.DAT.*
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11: /SIDS2/gcgdata/geneseq/geneseq/AA1990.DAT.*
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16: /SIDS2/gcgdata/geneseq/geneseq/AA1995.DAT.*
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19: /SIDS2/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq/AA2001.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1220	100.0	234	14 AAR45009	Sequence encoded b
2	1118	91.6	215	14 AAR45007	Sequence encoded b
3	860.5	70.5	239	14 AAR45008	Sequence encoded b
4	814.5	66.8	220	14 AAR45006	Sequence encoded b
5	741	60.7	143	21 AAB08276	Amino acid sequenc
6	608	49.8	143	21 AAB08277	Amino acid sequenc
7	115	9.4	279	17 AAR83357	Mouse Fas ligand.
8	112	9.2	179	16 AAR79069	Mouse Fas ligand (
9	112	9.2	279	16 AAR79098	Mouse Fas ligand.
10	108	8.9	143	21 AAB08266	Amino acid sequenc
11	106	8.7	138	16 AAR79068	Mouse Fas ligand (

12	104	8.5	137	16	AAR79067	Mouse Fas ligand (
13	102	8.4	279	16	AAR77282	Mouse Fas-L protei
14	97	8.0	268	19	AAW48953	Non-cleavable Fas
15	96.5	7.9	265	19	AAW48954	Non-cleavable Fas
16	95	7.8	180	18	AAW10875	FasL/IT-alpha hybr
17	94.5	7.7	281	22	AAU04556	Human Fas ligand p
18	93	7.6	216	19	AAW68412	Hybrid alpha-1-thy
19	92	7.5	378	18	AAW35864	Human Fas-Ligand: I
20	91.5	7.5	252	22	AAW66308	FasL fusion constr
21	91.5	7.5	261	20	AAW28597	Fas ligand (FasL)
22	91.5	7.5	281	21	AAW87581	Human Fas ligand (
23	91.5	7.5	376	21	AAW52588	Secreted modified
24	91	7.5	159	22	AAW66305	FasL fusion constr
25	91	7.5	258	20	AAW04371	Human Fas ligand d
26	90.5	7.4	145	18	AAW35848	Human Fas-Ligand f
27	90.5	7.4	151	18	AAW16667	Human Fas ligand (
28	90.5	7.4	178	16	AAW88308	C-terminally delet
29	90.5	7.4	179	16	AAW79099	Human Fas ligand (
30	90.5	7.4	179	18	AAW11814	Fas ligand. Homo
31	90.5	7.4	213	22	AAW66306	FasL fusion constr
32	90.5	7.4	213	22	AAW66307	FasL fusion constr
33	90.5	7.4	271	20	AAW28596	Fas ligand (FasL)
34	90.5	7.4	277	20	AAW28595	Fas ligand (FasL)
35	90.5	7.4	277	20	AAW04372	Human Fas ligand d
36	90.5	7.4	281	16	AAW77281	Human Fas-L protei
37	90.5	7.4	281	16	AAW79097	Human Fas ligand.
38	90.5	7.4	281	17	AAW98104	Human Fas ligand d
39	90.5	7.4	281	17	AAW88356	Human Fas ligand.
40	90.5	7.4	281	18	AAW27143	Human Fas ligand.
41	90.5	7.4	281	19	AAW75959	Human Fas ligand.
42	90.5	7.4	281	19	AAW49105	Fas Ligand. Mamma
43	90.5	7.4	281	20	AAW28594	Wild type Fas liga
44	90.5	7.4	281	20	AAW04373	Human Fas ligand d
45	90.5	7.4	281	20	AAW98071	Human Fas ligand (

ALIGNMENTS

RESULT 1
AAR45009
ID AAR45009 standard; Protein: 234 AA.
XX AC
XX AAR45009;
XX AC
DT 19-JUN-1994 (first entry)
XX Sequence encoded by a human CD30-L cDNA clone
DE encoding additional N-terminal amino acids.
XX
KW Hodgkin's disease; lymphoma; surface antigen; cytokine;
KW CD30 ligand; CD30-L; TNF; NGF.
XX Homo sapiens.
XX OS
XX Key Location/Qualifiers
FH Region 41..62
FT /label= Transmembrane
FT XX
XX WO9324135-A.
XX 09-DEC-1993.
XX 25-MAY-1993; 93WO-US04926.
XX 26-MAY-1992; 92US-0889717.
XX 02-JUN-1992; 92US-0892459.
XX 15-JUN-1992; 92US-0899660.
XX 01-JUL-1992; 92US-0907224.
XX 27-OCT-1992; 92US-0966775.
XX (IMMV) IMMUNEX CORP.

PI Armitage RJ, Goodwin RG, Smith CA;
 XX WPI: 1993-405417/50.
 DR N-PSDB; AAQ53538.
 XX
 DR New cytokine, CD30-L, which binds CD30 - used for developing
 PT prods. for diagnosis, detection, purifications, research and
 PT therapy
 XX
 PS Claim 15; Figure 7a; 59pp; English.
 XX
 CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
 CC as a clinical marker for Hodgkin's lymphoma and related haematologic
 CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
 CC L and other derived prods. can be used for elucidating the roles
 CC that CD30 and CD30-L may play in the immune system and for diagnosis
 CC and therapy. It can be isolated as follows. A cDNA library prepd. from
 CC the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion
 CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L
 CC (AAQ53535). This cDNA can then be used as a probe to screen a human PBL
 CC cDNA library to obtain cDNA encoding human CD30-L (AAQ53536). An
 CC anchored PCR technique was employed to isolate CD30-L human and murine
 CC clones containing an additional 19 N-terminal amino acid sequence
 CC (AAQ53537, AAQ53538).
 XX
 SQ Sequence 234 AA;
 Query Match 100.0%; Score 1220; DB 14; Length 234;
 Best Local Similarity 100.0%; Pred. No. 4,1e-124;
 Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDPLGQALNGMAPPDGTAMHVPAGSVASHLGTTSRSYFYLTTATLALCLVFTVATIMVL 60
 DB 1 mdplgqalngmappdgtamhvpagsvashlgttsrlyfytatlaiclvftvatimvl 60
 QY 61 VVQRTSDIPNSPDNVLKGGNCSDLLCILKRAPFKKSWAYLQVAKHLNKTLSWNRDGI 120
 DB 61 vvqrtsdipnsdpnvlkgnscsdllcilkrappfkkswaylvakhlntklswnkdgi 120
 QY 121 LHGVRYQDGNLVTFQFGLYFIICQLQFLVOCPPNNSVDLKEILLINKHKKOALVTVCESG 180
 DB 121 lhgvryqdgnlvtfqfglyfiicqlqflvqcpnnsvdlkelllnkhkkqalvtcesg 180
 QY 181 MQTKHYVQNLQFLLDYLVQNTTISVNVDTFOYIDTSTFPLENVLSIFLYSNSD 234
 DB 181 mqtkhyvqnlsqflldylvqnttisvndtfqyidstfplenvlsiflysnsd 234
 RESULT 2
 AAR45007
 ID AAR45007 standard; Protein; 215 AA.
 XX
 XX AAR45007;
 XX
 DT 19-JUN-1994 (first entry)
 XX
 DE Sequence encoded by a human CD30-L cDNA clone.
 XX
 KW Hodgkin's disease; lymphoma; surface antigen; cytokine;
 KW CD30 ligand; CD30-L; TNF; NGF.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Region 22..43
 FT /label= transmembrane
 XX
 XX W09324135-A.
 XX
 PD 09-DEC-1993.
 XX
 XX 25-MAY-1993; 93WO-US04926.

XX 26-MAY-1992; 92US-0889717.
 PR 02-JUN-1992; 92US-0892459.
 PR 15-JUN-1992; 92US-0895660.
 PR 01-JUL-1992; 92US-0907224.
 PR 27-OCT-1992; 92US-0966775.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Armitage RJ, Goodwin RG, Smith CA;
 XX
 DR WPI: 1993-405417/50.
 DR N-PSDB; AAQ53536.
 XX
 PT New cytokine, CD30-L, which binds CD30 - used for developing
 PT prods. for diagnosis, detection, purifications, research and
 PT therapy
 XX
 PS Claim 15; Figure 5a; 59pp; English.
 XX
 CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
 CC as a clinical marker for Hodgkin's lymphoma and related haematologic
 CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
 CC L and other derived prods. can be used for elucidating the roles
 CC that CD30 and CD30-L may play in the immune system and for diagnosis
 CC and therapy. It can be isolated as follows. A cDNA library prepd. from
 CC the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion
 CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L.
 CC This cDNA can then be used as a probe to screen a human PBL cDNA
 CC library to obtain cDNA encoding human CD30-L.
 XX
 SQ Sequence 215 AA;
 Query Match 91.6%; Score 1118; DB 14; Length 215;
 Best Local Similarity 100.0%; Pred. No. 4.2e-113;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 20 MHVPAGSVASHLGTTSRSYFYLTTATLALCLVFTVATIMVLVQRTSDIPNSPDNVLK 79
 DB 1 mhvpagsvashlgttsrlyfytatlaiclvftvatimlvvqrtsdipnsdpnvlk 60
 QY 80 GNCSDLLCILKRAPFKKSWAYLQVAKHLNKTLSWNRDGIHGVRYQDGNLVTFQFGLY 139
 DB 61 gncsdllcilkrappfkkswaylvakhlntklswnkdgilhgvryqdgnlvtfqfgy 120
 QY 140 FIICQLQFLVOCPPNNSVDLKEILLINKHKKOALVTVCESGMQTKHYVQNLQFLLDY 199
 DB 121 fiicqlqflvqcpnnsvdlkelllnkhkkqalvtcesgmqtkhyvqnlsqflldyl 180
 QY 200 VNTTISVNVDTFOYIDTSTFPLENVLSIFLYSNSD 234
 DB 181 vnttisvndtfqyidstfplenvlsiflysnsd 215
 RESULT 3
 AAR45008
 ID AAR45008 standard; Protein; 239 AA.
 XX
 XX AAR45008;
 XX
 DT 19-JUN-1994 (first entry)
 XX
 DE Sequence encoded by a murine CD30-L cDNA clone
 DE encoding additional N-terminal amino acids.
 XX
 KW Hodgkin's disease; lymphoma; surface antigen; cytokine;
 KW CD30 ligand; CD30-L; TNF; NGF.
 XX
 OS Acomys cahirinus.
 XX
 XX Key Location/Qualifiers
 FT Region 47..67

FT XX /label= Transmembrane

PN W09324135-A.

XX 09-DEC-1993.

XX 25-MAY-1993; 93WO-US04926.

XX 26-MAY-1992; 92US-0889717.

PR 02-JUN-1992; 92US-0892459.

PR 15-JUN-1992; 92US-0899660.

PR 01-JUL-1992; 92US-0907224.

PR 27-OCT-1992; 92US-0966775.

XX (IMMV) IMMUNEX CORP.

XX Armitage RJ, Goodwin RG, Smith CA;

XX WPI: 1993-405417/50.

XX N-PSDB; AAQ53537.

XX New cytokine, CD30-L, which binds CD30 - used for developing

XX prods. for diagnosis, detection, purifications, research and

XX therapy

XX Claim 15; Figure 6a; 59pp; English.

XX CD30-L is a ligand for CD30, the 120kd surface antigen widely used

XX as a clinical marker for Hodgkin's lymphoma and related haematologic

XX malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-

XX L and other derived prods. can be used for elucidating the roles

XX that CD30 and CD30-L may play in the immune system and for diagnosis

XX and therapy. It can be isolated as follows. A cDNA library prep. from

XX the murine helper T-cell line 7B9 is screened with a CD30/FC fusion

XX protein labelled with (125)I to obtain cDNA encoding murine CD30-L

XX (AAQ53537). This cDNA can then be used as a probe to screen a human PBL

XX cDNA library to obtain cDNA encoding human CD30-L (AAQ53536). An

XX anchored PCR technique was employed to isolate CD30-L human and murine

XX clones containing an additional 19 N-terminal amino acid sequence

XX (AAQ53537, AAQ53538).

XX Sequence 239 AA;

XX Query Match 70.5%; Score 860.5; DB 14; Length 239;

XX Best Local Similarity 69.6%; Pred No. 4.3e-85;

XX Matches 167; Conservative 28; Mismatches 38; Indels 7; Gaps 2;

XX 1 MDPGLQALNGMAPPGDTAMHPAGSVAS-----HLGTTSRSYFYLTATLALCLVFTV 54

XX 1 mepglqagscgapdpdpmqpgsvasprwtrstsrstsfylsttal-vclvvav 59

XX 55 ATIMVLVQRTDSIPNSPDNVLKGNCSDDLILKRAPFKKSWAYLOVAKHLNKTLS 114

XX 60 aailvlvqkdstpnttekaplkgncsedlftlktstpskkswaylqvskhlntkls 119

XX 115 WNKDGLHGVRYQDGNLVITQFGLYFIICQLQFLVQCPNNSVDLKLLELLINKHKKQALV 174

XX 120 wnedctingilvqgnlilvfpfilyfivcqlfivqcsnhsvdltlqlinskikkqtlv 179

XX 175 TVCESGMOTKHVYQNLSQLLDLYQVNTTISVNVDTFOYIDTSTFPLENVLISFLYSNSD 234

XX 180 tvcesgvskniyqnlsqlfllhylvqvnstisvrvdnfgyvdtntfpldnvlsvflysssd 239

DE XX Sequence encoded by a murine CD30-L cDNA clone.

KW Hodgkin's disease; lymphoma; surface antigen; cytokine;

KW CD30 ligand; CD30-L; TNF; NGF.

XX Acomys cahirinus.

XX Key Location/Qualifiers

XX Region 28..48

XX /label= transmembrane

XX W09324135-A.

XX 09-DEC-1993.

XX 25-MAY-1993; 93WO-US04926.

XX 26-MAY-1992; 92US-0889717.

XX 02-JUN-1992; 92US-0892459.

XX 15-JUN-1992; 92US-0899660.

XX 01-JUL-1992; 92US-0907224.

XX 27-OCT-1992; 92US-0966775.

XX (IMMV) IMMUNEX CORP.

XX Armitage RJ, Goodwin RG, Smith CA;

XX WPI: 1993-405417/50.

XX N-PSDB; AAQ53535.

XX New cytokine, CD30-L, which binds CD30 - used for developing

XX prods. for diagnosis, detection, purifications, research and

XX therapy

XX Claim 15; Figure 3a; 59pp; English.

XX CD30-L is a ligand for CD30, the 120kd surface antigen widely used

XX as a clinical marker for Hodgkin's lymphoma and related haematologic

XX malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-

XX L and other derived prods. can be used for elucidating the roles

XX that CD30 and CD30-L may play in the immune system and for diagnosis

XX and therapy. It can be isolated as follows. A cDNA library prep. from

XX the murine helper T-cell line 7B9 is screened with a CD30/FC fusion

XX protein labelled with (125)I to obtain cDNA encoding murine CD30-L.

XX This cDNA can then be used as a probe to screen a human PBL cDNA

XX library to obtain cDNA encoding human CD30-L.

XX Sequence 220 AA;

XX Query Match 66.8%; Score 814.5; DB 14; Length 220;

XX Best Local Similarity 70.6%; Pred. No. 3.7e-80;

XX Matches 136; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

XX 20 MHPVAGSVAS-----HLGTTSRSYFYLTATLALCLVFTVATIMVLVQRTDSIPNSPD 73

XX 1 mhpvagsvasprwtrstsrstsfylsttal-vclvvavailvlvqkdstpntte 59

XX 74 NVPLKGNCSDDLILKRAPFKKSWAYLOVAKHLNKTLSWNKDGILHGVRYQGNLVI 133

XX 60 kaplkgncsedlftlktstpskkswaylqvskhlntklswnedgtihgilyqgnlvi 119

XX 134 QFGLYFIICQLQFLVQCPNNSVDLKLLELLINKHKKQALVTCESGMOTKHVYQNLSQL 193

XX 120 qfpfilyfivcqlfivqcsnhsvdltlqlinskikkqtlvicesgvskniyqnlsql 179

XX RESULT 4

XX AAR45006

XX ID AAR45006 standard; Protein; 220 AA.

XX AC AAR45006;

XX 19-JUN-1994 (first entry)

XX DT

XX XX

```
ID  AAB08276 standard; Protein; 143 AA.
XX  AAB08276;
XX  04-DEC-2000 (first entry)
XX  Amino acid sequence of a human TNF ligand CD30L.
XX  AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;
XX  type II transmembrane protein; B cell stimulatory factor;
XX  inflammatory disorder; immune disorder; rheumatoid arthritis;
XX  lupus and graft versus host disease.
XX  Homo sapiens.
XX  WO200047740-A2.
XX  17-AUG-2000.
XX  11-FEB-2000; 2000WO-US03653.
XX  12-FEB-1999; 99US-0119906.
XX  18-NOV-1999; 99US-0166271.
XX  (AMGE-) AMGEN INC.
XX  Boyle WJ, Hsu H;
XX  WPI; 2000-558217/51.
XX  Novel polypeptides comprising tumour necrosis factor ligand family
XX  proteins, useful for treating inflammatory and immune disorders, e.g.
XX  rheumatoid arthritis -
XX  Claim 14; Fig 9; 7lpp; English.
XX  AAB08265-83 represent tumour necrosis factor (TNF) ligands. The
XX  specification describes an AGP-3 polypeptide, which is TNF ligand
XX  family member. AGP-3 is a type II transmembrane protein, and is a
XX  potent B cell stimulatory factor. Expression of AGP-3 correlates to
XX  increases in the number of B cells and immunoglobulins produced.
XX  AGP-3 proteins, antibodies, and nucleic acids may be used to treat
XX  inflammatory and immune disorders, e.g. rheumatoid arthritis,
XX  Crohn's disease, lupus and graft versus host disease. The nucleic
XX  acids may be used to regulate the expression of an AGP-3 related
XX  protein. The AGP-3 proteins, antibodies and nucleic acids are also
XX  useful for the detection of AGP-3 agonists, antagonists and
XX  characterizing interactions with AGP-3 related proteins.
XX  Sequence 143 AA;

Query Match 60.7%; Score 741; DB 21; Length 143;
Best Local Similarity 99.3%; Pred. No. 1.9e-72;
Matches 142; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 92 RAPEKSWAYLQVAKHLNKTLSWKNKGILHGVRYQDGNLVIOPPGLYFIICQLQFLVQC 151
Db 1 rapfkswaylqvakhlnktlswnkgilhgvrqdgnlviqpglyfiicqlqflvqc 60
QY 152 PNNVDLKLLELLINKHKIKQALVTVCSGMQTKHVYQNLQSQFLLDYLVQVNTTISVNDTF 211
Db 61 pnnsvdlklllnkhikqalvtvcsgmqtkhvyqnlqslqflldylqvnttisivndtf 120
QY 212 QYIDTSTFPLENVLSIFLYSNSD 234
Db 121 qyidststfplenvlsiflysnsd 143

RESULT 6
AAB08277
ID AAB08277 standard; Protein; 143 AA.
XX
```

```
AC AAB08277;
XX 04-DEC-2000 (first entry)
XX Amino acid sequence of a mouse TNF ligand CD30L.
XX AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;
XX type II transmembrane protein; B cell stimulatory factor;
XX inflammatory disorder; immune disorder; rheumatoid arthritis;
XX lupus and graft versus host disease.
XX Mus sp.
XX WO200047740-A2.
XX 17-AUG-2000.
XX 11-FEB-2000; 2000WO-US03653.
XX 12-FEB-1999; 99US-0119906.
XX 18-NOV-1999; 99US-0166271.
XX (AMGE-) AMGEN INC.
XX Boyle WJ, Hsu H;
XX WPI; 2000-558217/51.
XX Novel polypeptides comprising tumour necrosis factor ligand family
XX proteins, useful for treating inflammatory and immune disorders, e.g.
XX rheumatoid arthritis -
XX Claim 14; Fig 9; 7lpp; English.
XX AAB08265-83 represent tumour necrosis factor (TNF) ligands. The
XX specification describes an AGP-3 polypeptide, which is TNF ligand
XX family member. AGP-3 is a type II transmembrane protein, and is a
XX potent B cell stimulatory factor. Expression of AGP-3 correlates to
XX increases in the number of B cells and immunoglobulins produced.
XX AGP-3 proteins, antibodies, and nucleic acids may be used to treat
XX inflammatory and immune disorders, e.g. rheumatoid arthritis,
XX Crohn's disease, lupus and graft versus host disease. The nucleic
XX acids may be used to regulate the expression of an AGP-3 related
XX protein. The AGP-3 proteins, antibodies and nucleic acids are also
XX useful for the detection of AGP-3 agonists, antagonists and
XX characterizing interactions with AGP-3 related proteins.
XX Sequence 143 AA;

Query Match 49.8%; Score 608; DB 21; Length 143;
Best Local Similarity 78.0%; Pred. No. 5.1e-58;
Matches 110; Conservative 19; Mismatches 12; Indels 0; Gaps 0;

QY 94 PFKKSWAYLQVAKHLNKTLSWKNKGILHGVRYQDGNLVIOPPGLYFIICQLQFLVQC 153
Db 3 psfkswaylqvakhlnktlswnkgilhgvrqdgnlviqpglyfiicqlqflvqc 62
QY 154 NSVDLKLLELLINKHKIKQALVTVCSGMQTKHVYQNLQSQFLLDYLVQVNTTISVNDTF 213
Db 63 nsvdltlqlllnskkikqalvtvcsgmqtkhvyqnlqslqflldylqvnttisivndtf 122
QY 214 IDTSTFPLENVLSIFLYSNSD 234
Db 123 vdtstfplenvlsiflysnsd 143

RESULT 7
AAB8357
ID AAB8357 standard; Protein; 279 AA.
XX
XX AAB8357;
XX
```



```

DE Mouse Fas ligand (partial sequence).
KW Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;
KW Fas cell surface antigen; Fas-L; mouse.
XX
XX Mus musculus.
OS
XX
PN WO9513293-A1.
XX
XX 18-MAY-1995.
PD
XX
XX 10-NOV-1994; 94WO-JP01899.
PF
XX
XX 18-OCT-1994; 94JP-0278378.
PR
XX 10-NOV-1993; 93JP-0305975.
PR
XX 13-DEC-1993; 93JP-0342526.
PR
XX 18-MAR-1994; 94JP-0074344.
PR
XX 08-JUL-1994; 94JP-0180955.
PR
XX 07-SEP-1994; 94JP-0239363.
PF
XX
XX (MOCH ) MOCHIDA PHARM CO LTD.
PA
XX (OSAB-) OSAKA BIOSCIENCE INST.
XX
XX Nagata S, Nakamura N, Suda T, Takahashi T;
PI
XX WPI; 1995-194031/25.
DR
XX N-PSDB; AAQ99497.
XX
XX Peptide which binds to Fas antigen, and antibody reactive with it
PT for treatment and diagnosis of viral or auto:immune diseases
XX
XX Claim 10; Page 221-222; 300pp; Japanese.
XX
XX Fas ligands or active fragments able to induce apoptosis in cells
CC which express the Fas cell surface antigen are claimed. The
CC proteins are isolated from human, rat and mouse sources. The present
CC sequence represents part of the mouse Fas ligand.
XX
XX Sequence 138 AA;
SQ
Query Match 8.7%; Score 106; DB 16; Length 138;
Best Local Similarity 25.2%; Pred. No. 0.0014;
Matches 31; Conservative 22; Mismatches 46; Indels 24; Gaps 4;
QY 97 KSWAYLQVAKHLNKTLSWKNK---DGILHGVRVYQDGNLVLPFGGLYFIICQLQFLVQ-CP 152
Db 1 rsvahltgnphsrslplewedytgatllsgvkvkkgglvlnetglyfvyvskvyfrgscn 60
153 NNSVDLKLLELLINKH-----IKKQALVTVCESGM-----QTRKHVYQNLNQ 192
61 nqplnhkvmrnskydpdlvimeekrlncycttgqiwahssylgavfnltsadhlvynisq 120
QY 193 FLL 195
Db 121 lsl 123
RESULT 12
AAR79067
ID AAR79067 standard; Protein; 137 AA.
XX
XX AAR79067;
AC
XX
XX 22-FEB-1996 (first entry)
DT
XX
XX Mouse Fas ligand (partial sequence).
DE
XX
XX Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;
KW Fas cell surface antigen; Fas-L; mouse.
XX
XX Mus musculus.
OS
XX

```

```

PN WO9513293-A1.
XX
XX 18-MAY-1995.
PD
XX
XX 10-NOV-1994; 94WO-JP01899.
PF
XX
XX 18-OCT-1994; 94JP-0278378.
PR
XX 10-NOV-1993; 93JP-0305975.
PR
XX 13-DEC-1993; 93JP-0342526.
PR
XX 18-MAR-1994; 94JP-0074344.
PR
XX 08-JUL-1994; 94JP-0180955.
PR
XX 07-SEP-1994; 94JP-0239363.
PF
XX
XX (MOCH ) MOCHIDA PHARM CO LTD.
PA
XX (OSAB-) OSAKA BIOSCIENCE INST.
XX
XX Nagata S, Nakamura N, Suda T, Takahashi T;
PI
XX WPI; 1995-194031/25.
DR
XX N-PSDB; AAQ99496.
XX
XX Peptide which binds to Fas antigen, and antibody reactive with it
PT for treatment and diagnosis of viral or auto:immune diseases
XX
XX Claim 9; Page 219-221; 300pp; Japanese.
XX
XX Fas ligands or active fragments able to induce apoptosis in cells
CC which express the Fas cell surface antigen are claimed. The
CC proteins are isolated from human, rat and mouse sources. The present
CC sequence represents part of the mouse Fas ligand.
XX
XX Sequence 137 AA;
SQ
Query Match 8.5%; Score 104; DB 16; Length 137;
Best Local Similarity 25.4%; Pred. No. 0.0023;
Matches 31; Conservative 21; Mismatches 46; Indels 24; Gaps 4;
QY 98 SWAYLQVAKHLNKTLSWKNK---DGILHGVRVYQDGNLVLPFGGLYFIICQLQFLVQ-CPN 153
Db 1 svahltgnphsrslplewedytgatllsgvkvkkgglvlnetglyfvyvskvyfrgscn 60
154 NSVDLKLLELLINKH-----IKKQALVTVCESGM-----QTRKHVYQNLNQ 193
61 qpnhkvmrnskydpdlvimeekrlncycttgqiwahssylgavfnltsadhlvynisq 120
QY 194 LL 195
Db 121 sl 122
RESULT 13
AAR77282
ID AAR77282 standard; Protein; 279 AA.
XX
XX AAR77282;
AC
XX
XX 05-DEC-1995 (first entry)
DT
XX
XX Mouse Fas-L protein.
DE
XX
XX Fas ligand; Fas-L; cell surface protein; autoimmune disease;
KW self-tolerance.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
FH 1..78
FT Domain /label= Cytoplasmic_domain
FT Domain 79..103
FT Domain /label= Transmembrane_domain
FT Domain 104..279
FT Domain /label= Extracellular_domain
FT

```

XX WO9518819-A.
 XX 13-JUL-1995.
 XX 06-JAN-1995; 95WO-US00362.
 XX 01-FEB-1994; 94US-0190559.
 XX 07-JAN-1994; 94US-0179138.
 XX (IMV) IMMUNEX CORP.
 XX Goodwin RG;
 XX WPI; 1995-255032/33.
 XX N-PSDB; AAQ91312.
 XX Human and murine DNA encoding ligand(s) binding to cell surface protein
 XX Fas - useful for studying auto-immune disorder(s) and development of
 XX self-tolerance.
 XX Disclosure; Page 29-30; 38pp; English.
 XX A cDNA library prep'd. from mouse peripheral blood lymphocyte mRNA was
 XX screened with a murine Fas-L probe from the 3' end of Fas-L DNA.
 XX An isolated clone (AAQ91312) encoded mouse Fas-L.
 XX Sequence 279 AA;
 SQ
 Query Match 8.4%; Score 102; DB 16; Length 279;
 Best Local Similarity 22.9%; Pred. NO. 0.011;
 Matches 39; Conservative 28; Mismatches 57; Indels 46; Gaps 6;
 QY 52 FTVATIMLVVORTGIPNSPDVPLKGGNCSEDLICILKRAPFKKSWAYLQVAKHLNKT 111
 DB 115 ftnqslkvsfekiampstpe-----kkep--rsvahltnphrsi 156
 QY 112 KLSWNK---DGLHGVRYODGNLVIQFPGLYFIICQLQFLVQ-CPNNSVDLKLLELNKH 167
 DB 157 plwedtygtalisgvykkgglinetglyfvyyskvyfgrgscnqplnhkvymrnsy 216
 QY 168 IKKQALVTVCESGM-----QTKHVVYONLSQFL 195
 DB 217 --pedivlmeekrlnyftgtqiwahssyigavfnltsadhlyvnlsqsl 264
 RESULT 14
 ID AAW48953 standard; Protein; 268 AA.
 XX AAW48953;
 XX 23-SEP-1998 (first entry)
 XX Non-cleavable Fas ligand 1306142 deletion mutin.
 XX Non-cleavable Fas ligand 1306142 deletion mutin; Fas; erythematosis;
 XX gene therapy; autoimmune disease; multiple sclerosis;
 XX rheumatoid arthritis; myasthenia gravis; transplant rejection;
 XX glomerulonephritis.
 XX Homo sapiens.
 XX Synthetic.
 XX Key Location/Qualifiers
 XX Region 1..129
 XX /note= "represents residues 1-129 of the wild-type
 XX Fas ligand"
 XX Region 130..268
 XX /note= "represents residues 143-281 of the
 XX wild-type Fas ligand"
 XX

PN WO9821232-A2.
 PD 22-MAY-1998.
 XX 13-NOV-1997; 97WO-US20864.
 XX 12-NOV-1997; 97US-0968686.
 XX 13-NOV-1996; 96US-0030871.
 XX 10-FEB-1997; 97US-0039972.
 XX (CHIR) CHIRON CORP.
 XX Chu K;
 XX WPI; 1998-297861/26.
 XX N-PSDB; AAV32622.
 XX New DNA encoding Fas ligand agonist including, e.g. deletion -
 XX useful for, e.g. treating auto-immune diseases or transplant
 XX rejection
 XX Claim 4; Pages 62-63; 72pp; English.
 XX The present sequence represents a non-cleavable Fas ligand 1306142
 XX deletion mutin. Fas ligand deletion mutin can be expressed in
 XX cells transfected with the DNA (AAV32622) coding for the mutant protein.
 XX These cells, expressing the mutant Fas ligand in a non-cleavable form,
 XX are claimed to be useful in vitro to identify cells that express Fas
 XX and, in vivo or in vitro, for reducing proliferation of Fas-expressing
 XX cells. The DNA encoding the Fas ligand mutant is claimed to be
 XX useful in gene therapy procedures and for the treatment of autoimmune
 XX diseases, e.g. multiple sclerosis, erythematosis, rheumatoid arthritis,
 XX glomerulonephritis, myasthenia gravis and transplant rejection.
 XX Sequence 268 AA;
 SQ
 Query Match 8.0%; Score 97; DB 19; Length 268;
 Best Local Similarity 22.4%; Pred. NO. 0.035;
 Matches 45; Conservative 27; Mismatches 55; Indels 74; Gaps 9;
 QY 68 IPNSPDVPL-----KGCNSEDLLCIL-----KRA 93
 DB 54 lpppppppplpplpplkkrghnstg-lcllvmfmvalvlgiglmqfqlhqlkela 112
 QY 94 PFKXSWAYLQVAKHLNKT-----LSWNKD-GI--LHGVRYODGNLVIQF 135
 DB 113 elrestsqmhtassleklrvahlgtksnrsrsmplewedygvlslgvykkggline 172
 QY 136 PGLYFIICQLQFLVQ-CPNNSVDLKLLELNKH-----IKKQALVTVCESGM----- 181
 DB 173 tglyfvyyskvyfgrgscnplshkvymrnsykpqdlvmegkmmsycttgqmwarsyl 232
 QY 182 -----QTKHVVYONLSQFL 195
 DB 233 gavfnltsadhlyvnvselsl 253
 RESULT 15
 ID AAW48954 standard; Protein; 265 AA.
 XX AAW48954;
 XX 23-SEP-1998 (first entry)
 XX Non-cleavable Fas ligand 1306145 deletion mutin.
 XX Non-cleavable Fas ligand 1306145 deletion mutin; Fas; erythematosis;
 XX gene therapy; autoimmune disease; multiple sclerosis;
 XX rheumatoid arthritis; myasthenia gravis; transplant rejection;
 XX glomerulonephritis.
 XX

[illegible]

Search completed: January 22, 2002, 08:21:17
Job time: 302 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 22, 2002, 08:21:18 ; Search time 78.06 Seconds
(without alignments)
204.019 Million cell updates/sec

Title: US-09-628-126-23
Perfect score: 1118
Sequence: 1 MHPVAGSVASHLGTTSRSYF.....DTSTFPLENVLISFLYNSD 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SIDS2/gcgdata/geneseq/geneseq/AA2001.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1118	100.0	215	14 AAR45007	Sequence encoded b
2	1118	100.0	234	14 AAR45009	Sequence encoded b
3	814.5	72.9	220	14 AAR45006	Sequence encoded b
4	814.5	72.9	239	14 AAR45008	Sequence encoded b
5	741	66.3	143	21 AAB08276	Amino acid sequenc
6	608	54.4	143	21 AAB08277	Amino acid sequenc
7	115	10.3	279	17 AAR88357	Mouse Fas ligand.
8	112	10.0	279	16 AAR79069	Mouse Fas ligand (
9	112	10.0	279	16 AAR79098	Mouse Fas ligand.
10	108	9.7	143	21 AAB08266	Amino acid sequenc
11	106	9.5	138	16 AAR79068	Mouse Fas ligand (

12	104	9.3	137	16	AAR79067	Mouse Fas ligand (
13	102	9.1	279	16	AAR77282	Mouse Fas-L protei
14	97	8.7	268	19	AAW48953	Non-cleavable Fas
15	96.5	8.6	265	19	AAW48954	Non-cleavable Fas
16	95	8.5	180	18	AAW10875	FasL/Lt-alpha hybr
17	94.5	8.5	281	22	AAU04556	Human Fas ligand p
18	93	8.3	216	19	AAW68412	Hybrid alpha-1-thy
19	92	8.2	378	18	AAW35864	Human Fas-Ligand-I
20	91.5	8.2	252	22	AAW86308	FasL fusion constr
21	91.5	8.2	261	20	AAW28597	Fas ligand (FasL)
22	91.5	8.2	281	21	AAW87581	Human Fas ligand (
23	91.5	8.2	376	21	AAW52588	Secreted modified
24	91	8.1	159	22	AAW86305	FasL fusion constr
25	91	8.1	258	20	AAW04371	Human Fas ligand d
26	90.5	8.1	145	18	AAW35848	Human Fas-Ligand f
27	90.5	8.1	151	18	AAW16667	Human Fas ligand (
28	90.5	8.1	178	16	AAW88308	C-terminally delet
29	90.5	8.1	179	16	AAW79099	Human Fas ligand (
30	90.5	8.1	179	18	AAW11814	Fas ligand. Homo
31	90.5	8.1	213	22	AAW86306	FasL fusion constr
32	90.5	8.1	213	22	AAW86307	FasL fusion constr
33	90.5	8.1	271	20	AAW28596	Fas ligand (FasL)
34	90.5	8.1	277	20	AAW28595	Fas ligand (FasL)
35	90.5	8.1	277	20	AAW04372	Human Fas ligand d
36	90.5	8.1	281	16	AAW77281	Human Fas-L protei
37	90.5	8.1	281	16	AAW79097	Human Fas ligand.
38	90.5	8.1	281	17	AAW98104	Human Fas ligand d
39	90.5	8.1	281	17	AAW88356	Human Fas ligand.
40	90.5	8.1	281	18	AAW27143	Human Fas ligand.
41	90.5	8.1	281	19	AAW75959	Human Fas ligand.
42	90.5	8.1	281	19	AAW49105	Fas Ligand. Mamma
43	90.5	8.1	281	20	AAW28594	Wild type Fas liga
44	90.5	8.1	281	20	AAW04373	Human Fas ligand d
45	90.5	8.1	281	20	AAW98071	Human Fas ligand (

ALIGNMENTS

RESULT 1	
AAR45007	
ID AAR45007 standard; Protein; 215 AA.	
AC AAR45007;	
XX	
XX	
DT 19-JUN-1994 (first entry)	
XX	
DE Sequence encoded by a human CD30-L cDNA clone.	
XX	
KW Hodgkin's disease; lymphoma; surface antigen; cytokine;	
KW CD30 ligand; CD30-L; TNF; NGF.	
XX	
OS Homo sapiens.	
XX	
FH Key	Location/Qualifiers
FT Region	22..43
FT	/label- transmembrane
XX	
PN WO9324135-A.	
XX	
PD 09-DEC-1993.	
XX	
PF 25-MAY-1993;	93WO-US04926.
XX	
PR 26-MAY-1992;	92US-0889717.
PR 02-JUN-1992;	92US-0892459.
PR 15-JUN-1992;	92US-0899660.
PR 01-JUL-1992;	92US-0907224.
PR 27-OCT-1992;	92US-0966775.
XX	
PA (IMMV) IMMUNEX CORP.	
XX	
PI Armitage RJ, Goodwin RG, Smith CA;	

```

XX
DR 15-JUN-1992; 92US-0899660.
DR 01-JUL-1992; 92US-0907224.
XX 27-OCT-1992; 92US-0966775.
XX (IMNV ) IMMUNEX CORP.
XX
XX Armitage RJ, Goodwin RG, Smith CA;
XX
XX WPI; 1993-405417/50.
XX N-PSDB; AAQ53538.
XX
XX CD30-L is a ligand for CD30, the 120kd surface antigen widely used
XX as a clinical marker for Hodgkin's lymphoma and related haematologic
XX malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
XX L and other derived prods. can be used for elucidating the roles
XX that CD30 and CD30-L may play in the immune system and for diagnosis
XX and therapy. It can be isolated as follows. A cDNA library prepd. from
XX the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion
XX protein labelled with (125)I to obtain cDNA encoding murine CD30-L.
XX This cDNA can then be used as a probe to screen a human PBL cDNA
XX library to obtain cDNA encoding human CD30-L.
XX
XX Sequence 215 AA;
XX
XX Query Match 100.0%; Score 1118; DB 14; Length 215;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-116;
XX Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMLVVQRTDSIPNSPDNVLPG 60
XX Db 1 mhvpagsvashlgttsrsfylyttatlaclclvftvatimlvvqrdtsipnsdpnvlpg 60
XX
XX QY 61 GNCSEDLILCKRAPFKKSWAYLQVAKHLNKTLSWKNKGILHGVRYQDGNLVITQFPGLY 120
XX Db 61 gncsedlilckrapfkkswaylqvakhlnktlswknkgilhgvryqdgndlvitqfpgly 120
XX
XX QY 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKIKKQALVTVCESGMQTKHVVQNLSQFLDYLQ 180
XX Db 121 fiicqlqlvqcpcnnsvdllkllinkhkkqalvtvcsgmqtkhvyqnlsgflldylq 180
XX
XX QY 181 VNTTISVNVDTFOYIDTSTFPLENVLSIFLYSNSD 215
XX Db 181 vnttisvnnvdtfgyidstfplenvlsiflynsd 215
XX
XX RESULT 2
XX AAR45009
XX ID AAR45009 standard; Protein; 234 AA.
XX
XX AC AAR45009;
XX
XX 19-JUN-1994 (first entry)
XX
XX Sequence encoded by a human CD30-L cDNA clone
XX encoding additional N-terminal amino acids.
XX
XX Hodgkin's disease; lymphoma; surface antigen; cytokine;
XX CD30 ligand; CD30-L; TNF; NGF.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Region 41..62
XX FT /label= Transmembrane
XX
XX W09324135-A.
XX
XX 09-DEC-1993.
XX
XX 25-MAY-1993; 93WO-US04926.
XX
XX 26-MAY-1992; 92US-0889717.
XX 02-JUN-1992; 92US-0892459.

```

```

PR 15-JUN-1992; 92US-0899660.
PR 01-JUL-1992; 92US-0907224.
PR 27-OCT-1992; 92US-0966775.
XX
XX (IMNV ) IMMUNEX CORP.
XX
XX Armitage RJ, Goodwin RG, Smith CA;
XX
XX WPI; 1993-405417/50.
XX N-PSDB; AAQ53538.
XX
XX New cytokine, CD30-L, which binds CD30 - used for developing
XX prods. for diagnosis, detection, purifications, research and
XX therapy
XX
XX Claim 15; Figure 7a; 59pp; English.
XX
XX CD30-L is a ligand for CD30, the 120kd surface antigen widely used
XX as a clinical marker for Hodgkin's lymphoma and related haematologic
XX malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
XX L and other derived prods. can be used for elucidating the roles
XX that CD30 and CD30-L may play in the immune system and for diagnosis
XX and therapy. It can be isolated as follows. A cDNA library prepd. from
XX the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion
XX protein labelled with (125)I to obtain cDNA encoding murine CD30-L
XX (AAQ53538). This cDNA can then be used as a probe to screen a human PBL
XX cDNA library to obtain cDNA encoding human CD30-L (AAQ53538). An
XX anchored PCR technique was employed to isolate CD30-L human and murine
XX clones containing an additional 19 N-terminal amino acid sequence
XX (AAQ53537, AAQ53538).
XX
XX Sequence 234 AA;
XX
XX Query Match 100.0%; Score 1118; DB 14; Length 234;
XX Best Local Similarity 100.0%; Pred. No. 2.5e-116;
XX Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMLVVQRTDSIPNSPDNVLPG 60
XX Db 20 mhvpagsvashlgttsrsfylyttatlaclclvftvatimlvvqrdtsipnsdpnvlpg 79
XX
XX QY 61 GNCSEDLILCKRAPFKKSWAYLQVAKHLNKTLSWKNKGILHGVRYQDGNLVITQFPGLY 120
XX Db 80 gncsedlilckrapfkkswaylqvakhlnktlswknkgilhgvryqdgndlvitqfpgly 139
XX
XX QY 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKIKKQALVTVCESGMQTKHVVQNLSQFLDYLQ 180
XX Db 140 fiicqlqlvqcpcnnsvdllkllinkhkkqalvtvcsgmqtkhvyqnlsgflldylq 199
XX
XX QY 181 VNTTISVNVDTFOYIDTSTFPLENVLSIFLYSNSD 215
XX Db 200 vnttisvnnvdtfgyidstfplenvlsiflynsd 234
XX
XX RESULT 3
XX AAR45006
XX ID AAR45006 standard; Protein; 220 AA.
XX
XX AC AAR45006;
XX
XX 19-JUN-1994 (first entry)
XX
XX Sequence encoded by a murine CD30-L cDNA clone.
XX
XX Hodgkin's disease; lymphoma; surface antigen; cytokine;
XX CD30 ligand; CD30-L; TNF; NGF.
XX
XX Acomys cahirinus.
XX
XX Key Location/Qualifiers
XX FT Region 28..48
XX FT /label= transmembrane

```

```
XX PN WO9324135-A.
XX PD
XX PF 09-DEC-1993.
XX PT 25-MAY-1993; 93WO-US04926.
XX PR 26-MAY-1992; 92US-0889717.
XX PR 02-JUN-1992; 92US-0892459.
XX PR 15-JUN-1992; 92US-0899660.
XX PR 01-JUL-1992; 92US-0907224.
XX PR 27-OCT-1992; 92US-0966775.
XX PA (IMMV ) IMMUNEX CORP.
XX PI Armitage RJ, Goodwin RG, Smith CA;
XX PI WPI; 1993-405417/50.
XX DR N-PSDB; AAQ53535.
XX PT New cytokine, CD30-L, which binds CD30 - used for developing
XX PT prods. for diagnosis, detection, purifications, research and
XX PT therapy
XX PS Claim 15; Figure 3a; 59pp; English.
XX CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
XX CC as a clinical marker for Hodgkin's lymphoma and related haematologic
XX CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
XX CC L and other derived prods. can be used for elucidating the roles
XX CC that CD30 and CD30-L may play in the immune system and for diagnosis
XX CC and therapy. It can be isolated as follows. A cdna library prepd. from
XX CC the murine helper T-cell line 7B9 is screened with a CD30/FC fusion
XX CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L.
XX CC This cDNA can then be used as a probe to screen a human PBL cdna
XX CC library to obtain cDNA encoding human CD30-L.
XX SQ Sequence 220 AA;
Query Match 72.9%; Score 814.5; DB 14; Length 220;
Best Local Similarity 70.6%; Pred. No. 1.5e-82;
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;
QY 1 MHPVAGSVAS-----HLGTTSRSYFYLTATLALCLVFTVATIMLVVQRTDSIPNSPD 54
DB 1 mqvpgsvasprwstrprwstrsrsfyfisttal-vclvvavaillvqvkkdstpttte 59
QY 55 NVPLKGGNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSWKNKDGILHGVRVQDGNLVI 114
DB 60 kaplkgncsedlftclktstpskkswaylqvsqhlnntklswnedgtihglyqdggnliv 119
QY 115 QPGLYFIICQLQFLVQCPNNSVDLKLLELLINKHKQALVTVCSGMOTKHVYQNLVSQF 174
DB 120 qfpglyfivcqlqflvqcsnhsvdltqlqllnskkkqtlvtvcsgsvqskniyqnlsgf 179
QY 175 LLDYLVQVNTTISVNDTFQYIDTSTFPLENVLISFLYSNSD 215
DB 180 llhylvqvnstisvrndnfqyvdntfpldnvlsvflysssd 220
RESULT 4
AAR45008
ID AAR45008 standard; Protein; 239 AA.
XX AC AAR45008;
XX DT 19-JUN-1994 (first entry)
XX DE Sequence encoded by a murine CD30-L cdna clone
XX DE encoding additional N-terminal amino acids.
XX KW Hodgkin's disease; lymphoma; surface antigen; cytokine;
```

```
KW CD30 ligand; CD30-L; TNF; NGF.
XX Acomys cahirinus.
XX FH Key Location/Qualifiers
XX FT Region 47..67
XX FT /label= Transmembrane
XX PN WO9324135-A.
XX PD 09-DEC-1993.
XX PF 25-MAY-1993; 93WO-US04926.
XX PR 26-MAY-1992; 92US-0889717.
XX PR 02-JUN-1992; 92US-0892459.
XX PR 15-JUN-1992; 92US-0899660.
XX PR 01-JUL-1992; 92US-0907224.
XX PR 27-OCT-1992; 92US-0966775.
XX PA (IMMV ) IMMUNEX CORP.
XX PI Armitage RJ, Goodwin RG, Smith CA;
XX PI WPI; 1993-405417/50.
XX DR N-PSDB; AAQ53537.
XX PT New cytokine, CD30-L, which binds CD30 - used for developing
XX PT prods. for diagnosis, detection, purifications, research and
XX PT therapy
XX PS Claim 15; Figure 6a; 59pp; English.
XX CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
XX CC as a clinical marker for Hodgkin's lymphoma and related haematologic
XX CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
XX CC L and other derived prods. can be used for elucidating the roles
XX CC that CD30 and CD30-L may play in the immune system and for diagnosis
XX CC and therapy. It can be isolated as follows. A cdna library prepd. from
XX CC the murine helper T-cell line 7B9 is screened with a CD30/FC fusion
XX CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L
XX CC (AAQ53535). This cDNA can then be used as a probe to screen a human PBL
XX CC cdna library to obtain cDNA encoding human CD30-L (AAQ53536). An
XX CC anchored PCR technique was employed to isolate CD30-L human and murine
XX CC clones containing an additional 19 N-terminal amino acid sequence
XX CC (AAQ53537, AAQ53538).
XX SQ Sequence 239 AA;
Query Match 72.9%; Score 814.5; DB 14; Length 239;
Best Local Similarity 70.6%; Pred. No. 1.7e-82;
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;
QY 1 MHPVAGSVAS-----HLGTTSRSYFYLTATLALCLVFTVATIMLVVQRTDSIPNSPD 54
DB 20 mqvpgsvasprwstrprwstrsrsfyfisttal-vclvvavaillvqvkkdstpttte 78
QY 55 NVPLKGGNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSWKNKDGILHGVRVQDGNLVI 114
DB 79 kaplkgncsedlftclktstpskkswaylqvsqhlnntklswnedgtihglyqdggnliv 138
QY 115 QPGLYFIICQLQFLVQCPNNSVDLKLLELLINKHKQALVTVCSGMOTKHVYQNLVSQF 174
DB 139 qfpglyfivcqlqflvqcsnhsvdltqlqllnskkkqtlvtvcsgsvqskniyqnlsgf 198
QY 175 LLDYLVQVNTTISVNDTFQYIDTSTFPLENVLISFLYSNSD 215
DB 199 llhylvqvnstisvrndnfqyvdntfpldnvlsvflysssd 239
RESULT 5
AAB08276
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ID AAB08276 standard; Protein; 143 AA.
 AC AAB08276;
 XX
 DT
 XX
 DE
 XX
 DE
 XX
 XX
 Amino acid sequence of a human TNF ligand CD30L.
 KW AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;
 KW type II transmembrane protein; B cell stimulatory factor;
 KW inflammatory disorder; immune disorder; rheumatoid arthritis;
 KW lupus and graft versus host disease.
 XX
 OS
 XX
 OS
 XX
 Homo sapiens.
 XX
 PN
 PN
 WO200047740-A2.
 XX
 PD
 PD
 17-AUG-2000.
 XX
 PF
 PF
 11-FEB-2000; 2000WO-US03653.
 XX
 PR
 PR
 12-FEB-1999; 99US-0119906.
 XX
 PR
 PR
 18-NOV-1999; 99US-0166271.
 XX
 PA
 (AMGE-) AMGEN INC.
 XX
 PI
 PI
 Boyle WJ, Hsu H;
 XX
 XX
 WPI; 2000-558217/51.
 DR
 DR
 Novel polypeptides comprising tumour necrosis factor ligand family
 PT proteins, useful for treating inflammatory and immune disorders, e.g.
 PT rheumatoid arthritis -
 PT
 PT
 Claim 14; Fig 9; 7lpp; English.
 PS
 PS
 AAB08265-83 represent tumour necrosis factor (TNF) ligands. The
 CC specification describes an AGP-3 polypeptide, which is TNF ligand
 CC family member. AGP-3 is a type II transmembrane protein, and is a
 CC potent B cell stimulatory factor. Expression of AGP-3 correlates to
 CC increases in the number of B cells and immunoglobulins produced.
 CC AGP-3 proteins, antibodies, and nucleic acids may be used to treat
 CC inflammatory and immune disorders, e.g. rheumatoid arthritis,
 CC Crohn's disease, lupus and graft versus host disease. The nucleic
 CC acids may be used to regulate the expression of an AGP-3 related
 CC protein. The AGP-3 proteins, antibodies and nucleic acids are also
 CC useful for the detection of AGP-3 agonists, antagonists and
 CC characterizing interactions with AGP-3 related proteins.
 CC
 XX
 SQ
 Sequence 143 AA;
 Query Match 66.3%; Score 741; DB 21; Length 143;
 Best Local Similarity 99.3%; Pred. No. 1.3e-74;
 Matches 142; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 73 RAPFKKSWAYLQVAKHLNKTLSWKNKGILHGVRQDGNLVIOFPGLYFIICQLQFLVQC 132
 Db 1 rapfkkswaylvakhlntklswnkdgilhgvryqdgdnlviofpglyfiicqlqlvqc 60
 QY 133 PNNVDLKELELLINKHIKKOALVTVCESGMQTKHVYONLSQFLDYLQVNTTISVNVDTF 192
 Db 61 pnnsvdlikellinkhikqalvtvcsgmqtkhvyqnsqfildylqvmnttisvndtf 120
 QY 193 QYIDTSTFPLENVLSIFLYSNSD 215
 Db 121 qyidstfplenvlsiflysnsd 143
 RESULT 6
 AAB08277
 ID AAB08277 standard; Protein; 143 AA.
 XX

AC AAB08277;
 XX
 DT
 XX
 DE
 XX
 DE
 XX
 Amino acid sequence of a mouse TNF ligand CD30L.
 KW AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;
 KW type II transmembrane protein; B cell stimulatory factor;
 KW inflammatory disorder; immune disorder; rheumatoid arthritis;
 KW lupus and graft versus host disease.
 XX
 OS
 XX
 OS
 XX
 Mus sp.
 XX
 PN
 PN
 WO200047740-A2.
 XX
 PD
 PD
 17-AUG-2000.
 XX
 PF
 PF
 11-FEB-2000; 2000WO-US03653.
 XX
 PR
 PR
 12-FEB-1999; 99US-0119906.
 XX
 PR
 PR
 18-NOV-1999; 99US-0166271.
 XX
 PA
 (AMGE-) AMGEN INC.
 XX
 PI
 PI
 Boyle WJ, Hsu H;
 XX
 XX
 WPI; 2000-558217/51.
 DR
 DR
 Novel polypeptides comprising tumour necrosis factor ligand family
 PT proteins, useful for treating inflammatory and immune disorders, e.g.
 PT rheumatoid arthritis -
 PT
 PT
 Claim 14; Fig 9; 7lpp; English.
 PS
 PS
 AAB08265-83 represent tumour necrosis factor (TNF) ligands. The
 CC specification describes an AGP-3 polypeptide, which is TNF ligand
 CC family member. AGP-3 is a type II transmembrane protein, and is a
 CC potent B cell stimulatory factor. Expression of AGP-3 correlates to
 CC increases in the number of B cells and immunoglobulins produced.
 CC AGP-3 proteins, antibodies, and nucleic acids may be used to treat
 CC inflammatory and immune disorders, e.g. rheumatoid arthritis,
 CC Crohn's disease, lupus and graft versus host disease. The nucleic
 CC acids may be used to regulate the expression of an AGP-3 related
 CC protein. The AGP-3 proteins, antibodies and nucleic acids are also
 CC useful for the detection of AGP-3 agonists, antagonists and
 CC characterizing interactions with AGP-3 related proteins.
 CC
 XX
 SQ
 Sequence 143 AA;
 Query Match 54.4%; Score 608; DB 21; Length 143;
 Best Local Similarity 78.0%; Pred. No. 8.5e-60;
 Matches 110; Conservative 19; Mismatches 12; Indels 0; Gaps 0;
 QY 75 PFKKSWAYLQVAKHLNKTLSWKNKGILHGVRQDGNLVIOFPGLYFIICQLQFLVQC 134
 Db 3 pskkswaylvqskhlntklswnkdgilhgvryqdgdnlviofpglyfiicqlqlvqc 62
 QY 135 NSVDLKELELLINKHIKKOALVTVCESGMQTKHVYONLSQFLDYLQVNTTISVNVDTF 194
 Db 63 hsdvdtlqlllnskikqalvtvcsgvqskniyqnsqfildylqvnstisvrvdnfy 122
 QY 195 IDTSTFPLENVLSIFLYSNSD 215
 Db 123 vdtstfplenvlsiflysnsd 143
 RESULT 7
 AAB88357
 ID AAB88357 standard; Protein; 279 AA.
 XX
 AC
 AAB88357;
 XX

[illegible]

DE Mouse Fas ligand (partial sequence).
XX
KW Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;
KW Fas cell surface antigen; Fas-L; mouse.
XX
OS Mus musculus.
XX
PN WO9513293-A1.
XX
PD 18-MAY-1995.
XX
PF 10-NOV-1994; 94WO-JP01899.
XX
PR 18-OCT-1994; 94JP-0278378.
PR 10-NOV-1993; 93JP-0305975.
PR 13-DEC-1993; 93JP-0342526.
PR 18-MAR-1994; 94JP-0074344.
PR 08-JUL-1994; 94JP-0180955.
PR 07-SEP-1994; 94JP-0239363.
XX
PA (MOCH) MOCHIDA PHARM CO LTD.
PA (OSAB-) OSAKA BIOSCIENCE INST.
XX
PI Nagata S, Nakamura N, Suda T, Takahashi T;
XX WPI; 1995-194031/25.
DR N-PSDB; AAQ99497.
XX
PT Peptide which binds to Fas antigen, and antibody reactive with it
PT for treatment and diagnosis of viral or auto:immune diseases
XX
PS Claim 10; Page 221-222; 300pp; Japanese.
XX
CC Fas ligands or active fragments able to induce apoptosis in cells
CC which express the Fas cell surface antigen are claimed. The
CC proteins are isolated from human, rat and mouse sources. The present
CC sequence represents part of the mouse Fas ligand.
XX
SQ Sequence 138 AA;

Query Match 9.5%; Score 106; DB 16; Length 138;
Best Local Similarity 25.2%; Pred. No. 0.00072;
Matches 31; Conservative 22; Mismatches 46; Indels 24; Gaps 4;

Qy 78 KSWAYLQVAKHLNKTLSWKNK---DGILHGVRVQDGNLVIOFPGLYFIICQLQFLVO-CP 133
Db 1 rsvahltnphrsipledwtygtalishgkvkkgglvinetglyfyvyskvyfrgqscn 60
Qy 134 NNSVDLKLLELLINKH-----IKKQALVTVCESGM-----QTRKHVYONLSQ 173
Db 61 nqplnhkvmrnsypdvimeekrlnycttgqiwahssylgavfnltsadhlyvynisq 120

Qy 174 FLL 176
Db 121 lsl 123

RESULT 12
AAR79067
ID AAR79067 standard; Protein; 137 AA.
XX
AC AAR79067;
XX
DT 22-FEB-1996 (first entry)
XX
DE Mouse Fas ligand (partial sequence).
XX
KW Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;
KW Fas cell surface antigen; Fas-L; mouse.
XX
OS Mus musculus.

PN WO9513293-A1.
XX
PD 18-MAY-1995.
XX
PF 10-NOV-1994; 94WO-JP01899.
XX
PR 18-OCT-1994; 94JP-0278378.
PR 10-NOV-1993; 93JP-0305975.
PR 13-DEC-1993; 93JP-0342526.
PR 18-MAR-1994; 94JP-0074344.
PR 08-JUL-1994; 94JP-0180955.
PR 07-SEP-1994; 94JP-0239363.
XX
PA (MOCH) MOCHIDA PHARM CO LTD.
PA (OSAB-) OSAKA BIOSCIENCE INST.
XX
PI Nagata S, Nakamura N, Suda T, Takahashi T;
XX WPI; 1995-194031/25.
DR N-PSDB; AAQ99496.
XX
PT Peptide which binds to Fas antigen, and antibody reactive with it
PT for treatment and diagnosis of viral or auto:immune diseases
XX
PS Claim 9; Page 219-221; 300pp; Japanese.
XX
CC Fas ligands or active fragments able to induce apoptosis in cells
CC which express the Fas cell surface antigen are claimed. The
CC proteins are isolated from human, rat and mouse sources. The present
CC sequence represents part of the mouse Fas ligand.
XX
SQ Sequence 137 AA;

Query Match 9.3%; Score 104; DB 16; Length 137;
Best Local Similarity 25.4%; Pred. No. 0.0012;
Matches 31; Conservative 21; Mismatches 46; Indels 24; Gaps 4;

Qy 79 SWAYLQVAKHLNKTLSWKNK---DGILHGVRVQDGNLVIOFPGLYFIICQLQFLVO-CPN 134
Db 1 svahltnphrsipledwtygtalishgkvkkgglvinetglyfyvyskvyfrgqscn 60
Qy 135 NSVDLKLLELLINKH-----IKKQALVTVCESGM-----QTRKHVYONLSQF 174
Db 61 qpnhkvmrnsypdvimeekrlnycttgqiwahssylgavfnltsadhlyvynisq 120

Qy 175 LL 176
Db 121 sl 122

RESULT 13
AAR77282
ID AAR77282 standard; Protein; 279 AA.
XX
AC AAR77282;
XX
DT 05-DEC-1995 (first entry)
XX
DE Mouse Fas-L protein.
XX
KW Fas ligand; Fas-L; cell surface protein; autoimmune disease;
KW self-tolerance.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Domain 1..78
FT Domain /label= Cytoplasmic_domain
FT Domain 79..103
FT Domain /label= Transmembrane_domain
FT Domain 104..279
FT Domain /label= Extracellular_domain

XX WO9518819-A.
PN 13-JUL-1995.
XX
XX
XX 06-JAN-1995; 95WO-US00362.
XX
XX 01-FEB-1994; 94US-0190559.
PR 07-JAN-1994; 94US-0179138.
XX
XX (IMMUNEX CORP.
PA
XX
XX Goodwin RG;
PI
XX WPI; 1995-255032/33.
DR N-PSDB; AAQ91312.
XX
XX Human and murine DNA encoding ligand(s) binding to cell surface protein
Fas - useful for studying auto-immune disorder(s) and development of
self-tolerance.
XX
XX Disclosure; Page 29-30; 38pp; English.
PS
XX A cDNA library prepd. from mouse peripheral blood lymphocyte mRNA was
CC screened with a murine Fas-L probe from the 3' end of Fas-L DNA.
CC An isolated clone (AAQ91312) encoded mouse Fas-L.
XX
XX Sequence 279 AA;
SQ
Query Match 9.1%; Score 102; DB 16; Length 279;
Best Local Similarity 22.9%; Pred. No. 0.0055;
Matches 39; Conservative 28; Mismatches 57; Indels 46; Gaps 6;
QY 33 FTVATIMVLVORTDIPNSPDVPLKGGNCSEDLILKRAPFKKSWAYLQVAKHLNKT 92
DB 115 fnqslkvsfekqanptse-----kkep--rsvahltgnphrsi 156
QY 93 KLSWKN---DGLHGVRYODGNLVIQFPGLYFIICQLQFLVQ-CPNNSVDLKLLELNKH 148
DB 157 plewedytgaisgvykkggvlvnetglyfvyksvfyrgscnqpnkhkvmrnksy 216
QY 149 IKKQALVTVCESGM-----QTRHVVYQNLQSFL 176
DB 217 --pedivlmeekrlnyfttggihwahssylgavfnltsadhlyvnisqlsl 264
RESULT 14
AAW48953
ID AAW48953 standard; Protein; 268 AA.
XX
XX AAW48953;
AC
XX 23-SEP-1998 (first entry)
DT
XX Non-cleavable Fas ligand 1306142 deletion mutein.
DE
XX Non-cleavable Fas ligand 1306142 deletion mutein; Fas; erythematosis;
KW gene therapy; autoimmune disease; multiple sclerosis;
KW rheumatoid arthritis; myasthenia gravis; transplant rejection;
KW glomerulonephritis.
OS
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Region 1..129
FT /note= "represents residues 1-129 of the wild-type
FT Fas ligand"
FT 130..268
FT /note= "represents residues 143-281 of the
FT wild-type Fas ligand"
XX

PN WO9821232-A2.
XX
XX 22-MAY-1998.
XX
XX 13-NOV-1997; 97WO-US20864.
XX
XX 12-NOV-1997; 97US-0968686.
PR 13-NOV-1996; 96US-0030871.
PR 10-FEB-1997; 97US-0039972.
XX
XX (CHIR) CHIRON CORP.
PA
XX
XX Chu K;
PI
XX WPI; 1998-297861/26.
DR N-PSDB; AAV32622.
XX
XX New DNA encoding Fas ligand agonist including, e.g. deletion -
PT useful for, e.g. treating auto-immune diseases or transplant
PT rejection
XX
XX Claim 4; Pages 62-63; 72pp; English.
XX
XX The present sequence represents a non-cleavable Fas ligand 1306142
CC deletion mutein. Fas ligand deletion mutein can be expressed in
CC cells transfected with the DNA (AAV32622) coding for the mutant protein.
CC These cells, expressing the mutant Fas ligand in a non-cleavable form,
CC are claimed to be useful in vitro to identify cells that express Fas
CC and, in vivo or in vitro, for reducing proliferation of Fas-expressing
CC cells. The DNA encoding the Fas ligand mutant is claimed to be
CC useful in gene therapy procedures and for the treatment of autoimmune
CC diseases, e.g. multiple sclerosis, erythematosis, rheumatoid arthritis,
CC glomerulonephritis, myasthenia gravis and transplant rejection.
XX
SQ Sequence 268 AA;
Query Match 8.7%; Score 97; DB 19; Length 268;
Best Local Similarity 22.4%; Pred. No. 0.019;
Matches 45; Conservative 27; Mismatches 55; Indels 74; Gaps 9;
QY 49 IPNSPDVPL-----KGGNCSEDLILCIL-----KRA 74
DB 54 lpppppppplpplpplpkkrgnhstg-lcllvmfmfvmlvalvglgmfqihqkela 112
QY 75 PFKKSWAYLQVAKHLNKT-----LSWNKD-GI--LHGVRYODGNLVIQF 116
DB 113 elrestsqmhtassleklrkvahltgksnrsrsmplewedygvlvsgvykkggvlvne 172
QY 117 PGLYFIICQLQFLVQ-CPNNSVDLKLLELNKH-----IKKQALVTVCESGM-----162
DB 173 tglyfvyksvfyrgscnnpishkvmrnkskypqdlvmmegkmmssycttgqmwarsyl 232
QY 163 -----QTRHVVYQNLQSFL 176
DB 233 gavfnltsadhlyvnvselsl 253
RESULT 15
AAW48954
ID AAW48954 standard; Protein; 265 AA.
XX
XX AAW48954;
AC
XX 23-SEP-1998 (first entry)
DT
XX Non-cleavable Fas ligand 1306145 deletion mutein.
DE
XX Non-cleavable Fas ligand 1306145 deletion mutein; Fas; erythematosis;
KW gene therapy; autoimmune disease; multiple sclerosis;
KW rheumatoid arthritis; myasthenia gravis; transplant rejection;
KW glomerulonephritis.
XX

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OM protein - protein search, using sw model

Run on: January 22, 2002, 08:22:26 ; Search time 39.95 Seconds
(without alignments)
121.107 Million cell updates/sec

Title: US-09-628-126-23
Perfect score: 1118
Sequence: 1 MHPAGSVASHLGTTSRSYF.....DTSTFPLENVLISFLYNSD 215

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Minimum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1118	100.0	215	1 US-08-225-989-23	Sequence 23, Appl
2	1118	100.0	215	1 US-08-570-923-23	Sequence 23, Appl
3	1118	100.0	215	1 US-08-580-014-23	Sequence 23, Appl
4	1118	100.0	215	4 US-09-079-785-23	Sequence 23, Appl
5	1118	100.0	234	1 US-08-225-989-8	Sequence 8, Appli
6	1118	100.0	234	1 US-08-570-923-8	Sequence 8, Appli
7	1118	100.0	234	1 US-08-580-014-8	Sequence 8, Appli
8	1118	100.0	234	1 US-09-079-785-8	Sequence 8, Appli
9	814.5	72.9	220	1 US-08-225-989-19	Sequence 19, Appl
10	814.5	72.9	220	1 US-08-570-923-19	Sequence 19, Appl
11	814.5	72.9	220	4 US-08-580-014-19	Sequence 19, Appl
12	814.5	72.9	220	4 US-09-079-785-19	Sequence 19, Appl
13	814.5	72.9	239	1 US-08-225-989-6	Sequence 6, Appli
14	814.5	72.9	239	1 US-08-570-923-6	Sequence 6, Appli
15	814.5	72.9	239	1 US-08-580-014-6	Sequence 6, Appli
16	814.5	72.9	239	4 US-09-079-785-6	Sequence 6, Appli
17	775	69.3	148	3 US-08-584-031-12	Sequence 12, Appl
18	592	53.0	125	1 US-08-225-989-20	Sequence 20, Appl
19	592	53.0	125	1 US-08-570-923-20	Sequence 20, Appl
20	592	53.0	125	1 US-08-580-014-20	Sequence 20, Appl
21	592	53.0	125	4 US-09-079-785-20	Sequence 20, Appl
22	447.5	40.0	130	1 US-08-225-989-21	Sequence 21, Appl
23	447.5	40.0	130	1 US-08-570-923-21	Sequence 21, Appl
24	447.5	40.0	130	1 US-08-580-014-21	Sequence 21, Appl
25	447.5	40.0	130	4 US-09-079-785-21	Sequence 21, Appl
26	274	24.5	52	4 US-09-369-494-17	Sequence 17, Appl
27	274	24.5	52	4 US-09-358-569D-15	Sequence 15, Appl

28 102 9.1 279 5 PCT-US95-00362-5 Sequence 5, Appli
29 92 8.2 378 3 US-08-630-172-21 Sequence 21, Appl
30 92 8.2 378 3 US-09-375-419-21 Sequence 21, Appl
31 91.5 8.2 376 3 US-08-751-512-8 Sequence 8, Appli
32 90.5 8.1 145 4 US-08-630-172-5 Sequence 5, Appli
33 90.5 8.1 145 4 US-09-375-419-5 Sequence 5, Appli
34 90.5 8.1 179 3 US-08-649-100-9 Sequence 9, Appli
35 90.5 8.1 281 2 US-08-810-453-2 Sequence 2, Appli
36 90.5 8.1 281 3 US-08-815-190A-2 Sequence 2, Appli
37 90.5 8.1 281 4 US-09-290-640-25 Sequence 25, Appl
38 90.5 8.1 281 4 US-09-479-524-3 Sequence 3, Appli
39 90.5 8.1 281 5 PCT-US95-00362-2 Sequence 2, Appli
40 90.5 8.1 287 3 US-08-815-190A-16 Sequence 16, Appl
41 90 8.1 141 4 US-09-286-529-22 Sequence 22, Appl
42 90 8.1 149 3 US-08-584-031-17 Sequence 17, Appl
43 86 7.7 158 1 US-07-994-469A-99 Sequence 99, Appl
44 85.5 7.6 309 1 US-08-236-918A-2 Sequence 2, Appli
45 85 7.6 161 1 US-07-994-469A-61 Sequence 61, Appl

ALIGNMENTS

RESULT 1
US-08-225-989-23
; Sequence 23, Application US/08225989
; Patent No. 5480981

GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992

CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224

FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660

FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459

FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717

FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.

REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430

TELEFAX: (206)233-0644

```
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-225-989-23

Query Match 100.0%; Score 1118; DB 1; Length 215;
Best Local Similarity 100.0%; Pred. No. 6.3e-114;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVLPG 60
Db 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVLPG 60
61 GNCSEDLICILKRAPFKSWAYLOVAKHLNKTLSWKNKGILHGVRYODGNLVIQFPG 120
Db 61 GNCSEDLICILKRAPFKSWAYLOVAKHLNKTLSWKNKGILHGVRYODGNLVIQFPG 120
Qy 121 FIICQLQFLVQCPNNSVDLKLKLLINKHKIKKQALVTVCESGMOTKHVYQNLSQLDYLQ 180
Db 121 FIICQLQFLVQCPNNSVDLKLKLLINKHKIKKQALVTVCESGMOTKHVYQNLSQLDYLQ 180
Qy 181 VNTTISVNVDTFOYIDTSTFPLENVLSIFLYSNSD 215
Db 181 VNTTISVNVDTFOYIDTSTFPLENVLSIFLYSNSD 215

RESULT 2
US-08-570-923-23
; Sequence 23, Application US/08570923
; Patent No. 5677430
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,923
; FILING DATE: 12-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-570-923-23

Query Match 100.0%; Score 1118; DB 1; Length 215;
Best Local Similarity 100.0%; Pred. No. 6.3e-114;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVLPG 60
Db 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVLPG 60
61 GNCSEDLICILKRAPFKSWAYLOVAKHLNKTLSWKNKGILHGVRYODGNLVIQFPG 120
Db 61 GNCSEDLICILKRAPFKSWAYLOVAKHLNKTLSWKNKGILHGVRYODGNLVIQFPG 120
Qy 121 FIICQLQFLVQCPNNSVDLKLKLLINKHKIKKQALVTVCESGMOTKHVYQNLSQLDYLQ 180
Db 121 FIICQLQFLVQCPNNSVDLKLKLLINKHKIKKQALVTVCESGMOTKHVYQNLSQLDYLQ 180
Qy 181 VNTTISVNVDTFOYIDTSTFPLENVLSIFLYSNSD 215
Db 181 VNTTISVNVDTFOYIDTSTFPLENVLSIFLYSNSD 215

RESULT 3
US-08-580-014-23
; Sequence 23, Application US/08580014
; Patent No. 5753203
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Macintosh
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,014
; FILING DATE: 20-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
OM protein - protein search, using sw model
Run on: January 22, 2002, 08:17:43 ; Search time 55.1 Seconds
(without alignments)
323.500 Million cell updates/sec
Title: US-09-628-126-8
Perfect score: 1220
Sequence: 1 MDPGLQALNGMAPPGDTAM.....DTSTFPLENVLISFLYSNSD 234
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR_68: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1220	100.0	234	2 A40710	CD30 ligand - huma
2	860.5	70.5	239	2 B40710	CD30 ligand - mous
3	112	9.2	279	2 A53062	Fas ligand - mous
4	108.5	8.9	809	2 T38051	hypothetical prote
5	96.5	7.9	234	1 JQ1344	tumor necrosis fac
6	94	7.7	235	2 I54490	tumor necrosis fac
7	94	7.7	547	2 T30704	rifampicin resista
8	90.5	7.4	281	2 I38707	Fas ligand - human
9	90	7.4	233	1 S22052	tumor necrosis fac
10	87.5	7.2	813	2 T12506	hypothetical prote
11	86.5	7.1	3512	2 T17121	CPY protein - midg
12	86	7.0	278	2 A49266	fas ligand - rat
13	85.5	7.0	309	2 I53384	4-LBB ligand - mou
14	85	7.0	235	1 OMNSN	tumor necrosis fac
15	84.5	6.9	232	1 S12606	tumor necrosis fac
16	84	6.9	287	2 F81713	methylenetetrahydr
17	83.5	6.8	234	1 JH0529	tumor necrosis fac
18	83	6.8	636	2 S70877	hypothetical prote
19	83	6.8	1385	2 T18213	paraspinal crystal
20	82	6.7	513	2 B95524	hypothetical prote
21	82	6.7	1339	2 G84764	hypothetical prote
22	81.5	6.7	374	2 A71803	probable regulator
23	81.5	6.7	461	2 JN0129	ID-myo-inositol-tr
24	81	6.6	233	1 OHUN	tumor necrosis fac
25	81	6.6	547	2 H65107	hypothetical 61.6
26	81	6.6	1289	2 T18212	paraspinal crystal
27	80.5	6.6	434	2 T28318	ORF MSV157 hypothe
28	80.5	6.6	434	1 S61999	hypothetical prote
29	80.5	6.6	499	2 A55346	phosphoprotein pho

30	80	6.6	235	2 JU0029	tumor necrosis fac
31	79.5	6.5	233	1 S24642	tumor necrosis fac
32	79.5	6.5	5825	2 T12117	polyprotein - fava
33	79	6.5	372	2 D64716	regulatory protein
34	79	6.5	800	2 S53079	PEP11 protein - y
35	78.5	6.4	426	2 S64748	mitochondrial oute
36	78.5	6.4	1130	2 T29089	alpha-mannosidase
37	78.5	6.4	1830	2 E82909	conserved hypothet
38	77.5	6.4	492	2 S42735	cytochrome-c oxida
39	77.5	6.4	610	2 S71758	DEAD box protein M
40	77.5	6.4	623	2 B96681	F5114.14 [imported
41	77.5	6.4	829	2 S72366	DNA topoisomerase
42	77	6.3	329	2 T28412	ORF MSV251 hypothe
43	77	6.3	456	2 B96688	unknown protein, 1
44	76.5	6.3	478	2 T27714	hypothetical prote
45	76.5	6.3	619	2 S54636	probable membrane

ALIGNMENTS

RESULT 1
A40710
CD30 ligand - human
C:Species: Homo sapiens (man)
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 21-Jul-2000
C:Accession: A40710
R:Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah, T.; Baker, E.; Sutherland, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage, A.; Reference number: A40710; MUID:93313964
Cell 73, 1349-1360, 1993
A:Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de
A:Reference number: A40710; MUID:93313964
A:Accession: A40710
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-234 <SMI>
A:Cross-references: GB:L09753; NID:g349277; PIDN:AAA74594.1; PID:g349278
C:Keywords: cytokine receptor; membrane protein; surface antigen

Query Match 100.0%; Score 1220; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 5.7e-109;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDPGLQALNGMAPPGDTAMHVPAGSVASHLGTTSRSYFYLTTATLALCLVFTVATIMVL 60
DB 1 MDPGLQALNGMAPPGDTAMHVPAGSVASHLGTTSRSYFYLTTATLALCLVFTVATIMVL 60
QY 61 VVQRTDSIPNSPDNVPLKGGNCSEDLICILKRAPEKKSWAYLQVAKHLNKTLSNWKDGI 120
DB 61 VVQRTDSIPNSPDNVPLKGGNCSEDLICILKRAPEKKSWAYLQVAKHLNKTLSNWKDGI 120
QY 121 LHGVRYDGNLVIFPGGLYFIICQLQFLVQCPNNSVDLKLKLLINKHKKQALVTVCSG 180
DB 121 LHGVRYDGNLVIFPGGLYFIICQLQFLVQCPNNSVDLKLKLLINKHKKQALVTVCSG 180
QY 181 MÖTRHVYONLSQFLDYLVQVNTTISVNVDTFOYIDTSTFPLENVLISFLYSNSD 234
DB 181 MÖTRHVYONLSQFLDYLVQVNTTISVNVDTFOYIDTSTFPLENVLISFLYSNSD 234

RESULT 2
B40710
CD30 ligand - mouse
C:Species: Mus musculus (house mouse)
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999
C:Accession: B40710
R:Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah, T.; Baker, E.; Sutherland, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage, A.; Reference number: A40710; MUID:93313964
Cell 73, 1349-1360, 1993
A:Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de
A:Reference number: A40710; MUID:93313964
A:Accession: B40710

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 22, 2002, 08:31:34 ; Search time 33.56 Seconds
(without alignments)
255.649 Million cell updates/sec

Title: US-09-628-126-8

Perfect score: 1220

Sequence: 1 MDPGLQALNGMAPPDGTAM.....DTSTFPLENVLSIFLYSNSD 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1220	100.0	234	1	TNF8_HUMAN
2	860.5	70.5	239	1	TNF8_MOUSE
3	112	9.2	279	1	FASL_MOUSE
4	108.5	8.9	809	1	YATA_SCHPO
5	96.5	7.9	234	1	TNFA_HORSE
6	94	7.7	233	1	TNFA_MACMU
7	94	7.7	235	1	TNFA_PERLE
8	92	7.5	233	1	TNFA_MACFA
9	90.5	7.4	281	1	FASL_HUMAN
10	90	7.4	233	1	TNFA_PAPHU
11	90	7.4	233	1	TNFA_PAPSP
12	86	7.0	278	1	FASL_RAT
13	85.5	7.0	309	1	41BL_MOUSE
14	85	7.0	233	1	TNFA_CANFA
15	85	7.0	235	1	TNFA_MOUSE
16	85	7.0	1220	1	CSAC_BACTU
17	84.5	6.9	232	1	TNFA_PIG
18	83.5	6.8	234	1	TNFA_SHEEP
19	83	6.8	1385	1	CSAA_BACUD
20	81.5	6.7	461	1	IP3K_HUMAN
21	81	6.6	233	1	TNFA_HUMAN
22	81	6.6	233	1	TNFA_MARMO
23	81	6.6	541	1	YHXB_ECOLI
24	81	6.6	1289	1	CSAB_BACUD
25	80.5	6.6	499	1	PPP5_RAT
26	80	6.6	229	1	TNFA_CEREL
27	80	6.6	235	1	TNFA_RAT
28	79.5	6.5	233	1	TNFA_BOVIN
29	79	6.5	800	1	PT11_YEAST
30	78.5	6.4	424	1	TNFA_CAVPO
31	78.5	6.4	236	1	MMML_YEAST
32	77.5	6.4	670	1	DD18_HUMAN
33	77.5	6.4	829	1	TOP1_XENLA

34	76	6.2	479	1	PAP1_VACCC	P21079 vaccinia vi
35	76	6.2	982	1	MSHM_SARGL	O63852 sarcophyton
36	75.5	6.2	807	1	SUS1_ARATH	P49040 arabidopsis
37	75	6.1	427	1	SYS_BUCAP	P81434 buchnera ap
38	75	6.1	499	1	PPP5_HUMAN	P53041 homo sapien
39	74.5	6.1	745	1	RNR_BUCAI	P57628 buchnera ap
40	74	6.1	459	1	IP3K_RAT	P17105 rattus norv
41	74	6.1	541	1	YHXB_ECO57	P58216 escherichia
42	74	6.1	851	1	NUD1_YEAST	P32336 saccharomyc
43	74	6.1	1064	1	CY4A_RAT	P26770 rattus norv
44	74	6.1	2136	1	YCF2_MARPO	P09975 marchantia
45	73.5	6.0	1178	1	PH81_YEAST	P17442 saccharomyc

ALIGNMENTS

RESULT 1

ID	TNF8_HUMAN	STANDARD;	PRT;	234 AA.
AC	P32971;			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-OCT-1993 (Rel. 27, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	CD30 LIGAND (CD30-L) (CD153 ANTIGEN).			
GN	TNFSF8 OR CD30LG OR CD30L.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-93313964; PubMed-8391931;			
RA	Smith C.A., Gruess H.-J., Davis T., Anderson D., Farrah T.,			
RA	Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,			
RA	Grabstein K.H., Gliniak B., McAlister I.B., Fanslow W., Alderson M.,			
RA	Falk B., Gimpsey S., Gillis S., Din W.S., Goodwin R.G., Armitage R.J.;			
RT	"CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose			
RT	ligand defines an emerging family of cytokines with homology to			
RT	TNF".			
RL	Cell 73:1349-1360(1993).			
CC	-!- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF			
CC	T CELLS.			
CC	-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.			
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.			
CC	-!- DATABASE: NAME=PRO; NOTE=CD guide CD153 entry;			
CC	WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd153.htm".			
CC	-----			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: L09753; AAA74594.1; -			
DR	PIR; A40710; A40710.			
DR	MIM; 603875; -			
DR	InterPro; IPR003638; TNF_8.			
DR	InterPro; IPR000478; TNF_family.			
DR	Pfam; PF00229; TNF; 1.			
DR	ProDom; PD023087; TNF_8; 1.			
DR	SMART; SM00207; TNF; 1.			
DR	PROSITE; PS00251; TNF_1; 1.			
DR	PROSITE; PS00049; TNF_2; 1.			
KW	Cytokine; Transmembrane; Glycoprotein; Signal-anchor.			
FT	DOMAIN 1 37			
FT	TRANSMEM 38 62			
FT	DOMAIN 63 234			
FT	CARBOHYD 81 81			
FT	CARBOHYD 109 109			
FT	CARBOHYD 153 153			

FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 234 AA; 26017 MW; C653615682305B1B CRC64;

Query Match 100.0%; Score 1220; DB 1; Length 234;
 Best Local Similarity 100.0%; Pred. No. 8e-108; Indels 0; Gaps 0;
 Matches 234; Conservative 0; Mismatches 0;

OY 1 MDPGLQALNGMAPPDGTAMHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVL 60
 DB 1 MDPGLQALNGMAPPDGTAMHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVL 60

OY 61 VQRTSDIPNSPDNVLKGCNSEDLLILKRAPFKKSWAYLQVAKHLNKTLSWNRDGI 120
 DB 61 VQRTSDIPNSPDNVLKGCNSEDLLILKRAPFKKSWAYLQVAKHLNKTLSWNRDGI 120

OY 121 LHGVRVQDGNLVITQFGLYFIICQLQFLVQCPNNSVDLKLLELNKHKQALVTCESG 180
 DB 121 LHGVRVQDGNLVITQFGLYFIICQLQFLVQCPNNSVDLKLLELNKHKQALVTCESG 180

OY 181 MQTKHYQNLSQLLDYLVQNTTISVNVDTFOYIDTSTFPLENVLISFLYSNSD 234
 DB 181 MQTKHYQNLSQLLDYLVQNTTISVNVDTFOYIDTSTFPLENVLISFLYSNSD 234

RESULT 2
 TNF8_MOUSE
 ID TNF8_MOUSE STANDARD; PRT; 239 AA.
 AC P32972;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE CD30 LIGAND (CD30-L).
 GN TNFSF8 OR CD30LG OR CD30L.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=F-cell;
 RA Smith C.A., Gruess H.-J., Davis T., Anderson D., Farrah T.,
 Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,
 Grabstein K.H., Gliniak B., McAlister I.B., Fanslow W., Alderson M.,
 Falk B., Gimpel S., Gillis S., Din W.S., Goodwin R.G., Armitage R.J.;
 "CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose
 ligand defines an emerging family of cytokines with homology to
 TNF.";
 RL Cell 73:1349-1360(1993).
 CC -!- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF
 T CELLS.
 CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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 CC -----
 DR EMBL; L09754; AAA74595.1; -;
 DR PIR; B40710; B40710.
 DR MGD; MGI:88328; Tnfsf8.
 DR InterPro; IPR003638; TNF8.
 DR InterPro; IPR000478; TNF_family.
 DR Pfam; PF00229; TNF; 1.
 DR ProDom; PD023087; TNF; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.

DR PROSITE; PS50049; TNF_2; 1.
 KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
 FT DOMAIN 1 43 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 44 67 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT DOMAIN 68 239 EXTRACELLULAR (POTENTIAL).
 FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 239 AA; 26519 MW; 29003157DD425159 CRC64;

Query Match 70.5%; Score 860.5; DB 1; Length 239;
 Best Local Similarity 69.6%; Pred. No. 6.1e-74;
 Matches 167; Conservative 28; Mismatches 38; Indels 7; Gaps 2;

OY 1 MDPGLQALNGMAPPDGTAMHVPAGSVAS-----HLGTTTSRSFYLTATLALCLVFTV 54
 DB 1 MDPGLQALNGMAPPDGTAMHVPAGSVAS-----HLGTTTSRSFYLTATLALCLVFTV 54

OY 55 ATIMVLVQRTSDIPNSPDNVLKGCNSEDLLILKRAPFKKSWAYLQVAKHLNKTLS 114
 DB 60 ATIMVLVQRTSDIPNSPDNVLKGCNSEDLLILKRAPFKKSWAYLQVAKHLNKTLS 114

OY 115 WNKDGIHLGVRVQDGNLVITQFGLYFIICQLQFLVQCPNNSVDLKLLELNKHKQALV 174
 DB 120 WNKDGIHLGVRVQDGNLVITQFGLYFIICQLQFLVQCPNNSVDLKLLELNKHKQALV 174

OY 175 TVCESGMQTKHYQNLSQLLDYLVQNTTISVNVDTFOYIDTSTFPLENVLISFLYSNSD 234
 DB 180 TVCESGMQTKHYQNLSQLLDYLVQNTTISVNVDTFOYIDTSTFPLENVLISFLYSNSD 234

RESULT 3
 FASL_MOUSE
 ID FASL_MOUSE STANDARD; PRT; 279 AA.
 AC P41047; O61217; O9R1F2;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE FAS ANTIGEN LIGAND.
 GN TNFSF6 OR APTILG1 OR FASL OR GLD.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM FASL).
 RX MEDLINE=94185175; PubMed=7511063;
 RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
 Suda T., Nagata S.;
 RT "Generalized lymphoproliferative disease in mice, caused by a point
 mutation in the Fas ligand.";
 RL Cell 76:969-976(1994).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.
 RC STRAIN=C57BL/6;
 RX MEDLINE=95388076; PubMed=7544870;
 RA Peltsch M.J., Tschopp J.J.;
 RT "Comparative molecular modelling of the Fas-ligand and other members
 of the TNF family.";
 RL Mol. Immunol. 32:761-772(1995).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM FASL).
 RX MEDLINE=95196085; PubMed=7889405;
 RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
 Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
 RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a
 TNF family gene cluster.";
 RL Immunity 1:131-136(1994).
 RN [4]

ult No.	Score		Query Match	Length	DB	ID	Description
	8	9					
1	1196	98.0	234	4	043404	043404 homo sapien	
2	1100	8.2	169	11	Q9WV90	Q9WV90 marmota mon	
3	96.5	7.9	215	6	Q9BEE8	Q9BEE8 erinaceus e	
4	95.5	7.8	280	6	Q9BDN1	Q9BDN1 cercocebus	
5	94.5	7.7	234	6	Q9TTJ3	Q9TTJ3 equus cabal	
6	94	7.7	547	12	Q98269	Q98269 molluscum c	
7	93	7.6	217	11	Q9ERG6	Q9ERG6 peromyscus	
8	92	7.5	280	6	Q9MYL6	Q9MYL6 macaca neme	
9	92	7.5	280	6	Q9BDM5	Q9BDM5 macaca mula	
10	89.5	7.3	892	10	Q9S9U5	Q9S9U5 arabidopsis	
11	89.5	7.3	896	10	Q9M9B0	Q9M9B0 arabidopsis	
12	88.5	7.3	217	6	Q9BEG1	Q9BEG1 bradyopus tr	
13	88	7.2	1109	5	Q9GYH7	Q9GYH7 caenorhabdi	
14	87.5	7.2	216	6	Q9BEC4	Q9BEC4 talpa europ	
15	87.5	7.2	813	4	Q9Y4N0	Q9Y4N0 homo sapien	
16	87.5	7.2	1003	4	Q9P207	Q9P207 homo sapien	
17	87	7.1	462	2	Q9CM44	Q9CM44 pasteurella	
18	86.5	7.1	3512	6	Q62524	Q62524 chironomus	
19	85	7.0	282	6	Q9BEA8	Q9BEA8 sus scrofa	

|||||
Db 61 VVQRTDSIPSPDNVPLKGGNCSEDLCLILKRAPFKKSWAYLQVAKHLNKTLSWKNKGI 120
QY 121 LHGVRYQDGNLVIOFPGGLYFIICQLQFVQCPNNNSVDKLELLINKHKKQALVTVCESG 180
Db 121 LHGVRYQDGNLVIOFPGGLYFIICQLQFVQCPNNNSVDKLELLINKHKKQALVTVCESG 180
QY 181 MQTKHYQNLISQFLDYLVQNTTISVNVDTFOYIDTSTFFPLENVLSIFLXNSD 234
Db 181 MQTKHYQNLISQFLDYLVQNTTISVNVDTFOYIDTSTFFPLENVLSIFLXNSD 234
RESULT 2
Q9WV90 PRELIMINARY; PRT; 169 AA.
AC Q9WV90;
DT 01-NOV-1999 (T-EMBLrel. 12, Created)
DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE FAS LIGAND (FRAGMENT).
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Scurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEALTHY LIVER;
RA Hodgson P.D., Grant M.D., Michalak T.I.;
RT "Perforin and Fas/Fas ligand-mediated cytotoxicity in acute and
RT chronic woodchuck viral hepatitis.";
RL Clin. Exp. Immunol. 0:0-0(1999).
DR EMBL; AF152368; AAD38387.1; -
DR InterPro; IPR000478; TNE family.
DR InterPro; IPR003263; TNF_5.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD008600; TNF_5; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
DR SMART; SM00207; TNF; 1.
FT NON_TER 1 169
FT NON_TER 169 169
SQ SEQUENCE 169 AA; 19274 MW; FDE395B014717B6B CRC64;

Query Match 8.2%; Score 100; DB 11; Length 169;
Best Local Similarity 24.6%; Pred. No. 0.03;
Matches 32; Conservative 23; Mismatches 45; Indels 30; Gaps 5;
QY 90 LKRAPFKKSWAYLQVAKHLNKTLSWKNK---GLHGVRYQDGNLVIOFPGGLYFIICQLQ 146
Db 40 LRRA-----AHLTGKPNSSPSPLEWEDTYGISLSGVKYGKGLVINDTGLYFVYSKIY 93
QY 147 FLVQ-CPNNNSVDKLELLINKH-----IKQALVTVCESGM-----OTKH 185
Db 94 FQGSCNNQPLSHKVVYKNSKYPODLVLMGCKMMNYCTTGOMWARSSYLGVAFNFTSNDH 153
QY 186 VYQNLISQFL 195
Db 154 LYVNVSELSL 163

RESULT 3
Q9BEE8 PRELIMINARY; PRT; 215 AA.
AC Q9BEE8;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR PRECURSOR (FRAGMENT).
GN TNFA.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.
OX NCBI_TaxID=9365;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are
RT their sister group.";
RL submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286830; CAC28522.1; -
FT NON_TER 1 215
FT NON_TER 215 215
SQ SEQUENCE 215 AA; 23696 MW; 3E337E7E65F074EA CRC64;

Query Match 7.9%; Score 96.5; DB 6; Length 215;
Best Local Similarity 23.3%; Pred. No. 0.089;
Matches 47; Conservative 36; Mismatches 76; Indels 43; Gaps 10;
QY 37 SYFYLTATLALCLVFTVATIMVLVVQRTDSIPNSPDNVPKGGNCSEDLCLILK--RAP 94
Db 28 SFFLVAGATTFLCLLH---FCVIGPQRDE---FPDNIQLNNA-----LAQTLRSSRTQ 74
QY 95 FKKSWAYLQVAKHLNKTLSWKNKDG---ILHGVRYQDGNLVIOFPGGLYFIICQLQFLVQ 150
Db 75 SDKPVAVH-VASIKSEGQLLWSEVANALLANGMLTDNLVPLDGLYLYSQVLFKQG 133
QY 151 -CPNNNSVDKLELLINKHKIK-----QALVTVCES-----GMOTKHYVQNLISQF 193
Db 134 GCPSTHV-----FLTHNKRKRVAVSYQKDVNLLSAIKSPQSETPGAEARPWYFIYLG 187
QY 194 LLDYLQVNTTISVNVDTFOYID 215
Db 188 GVFOLEKGDRLSAEINLPDYLD 209

RESULT 4
Q9BDN1 PRELIMINARY; PRT; 280 AA.
AC Q9BDN1;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE CD95L PROTEIN.
GN CD95L.
OS Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Cercocebus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RA Villinger F., Bostlik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing and homology analysis of nonhuman primate
RT Fas/Fas-Ligand and co-stimulatory molecules.";
RL Immunogenetics 0:0-0(2001).
DR EMBL; AF344847; AAK37606.1; -
SQ SEQUENCE 280 AA; 31407 MW; 729EA60067B7D398 CRC64;

Query Match 7.8%; Score 95.5; DB 6; Length 280;
Best Local Similarity 27.18; Pred. No. 0.15;
Matches 35; Conservative 21; Mismatches 46; Indels 27; Gaps 6;
QY 94 PFKKS---AYLQVAKHLNKTLSWKNK-GI--LHGVRYQDGNLVIOFPGGLYFIICQLQF 147
Db 137 PEKKEQRKVAHLTGKPNSSPSPLEWEDTYGIVLLSGVKYKGLVNETGLYFVYSKVYF 196
QY 148 LVQ-CPNNNSVDKLELLINKH-----IKQALVTVCESGM-----OTKH 186
Db 197 RGQCTNPLPSHKVYMRNSKYPQDLVMMEGKMMSYCTTGOMWAHSSYLGVAFNLTSTDL 256
QY 187 YQNLISQFL 195

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OM protein - protein search, using sw model

Run on: January 22, 2002, 08:22:25 ; Search time 39.95 Seconds
(without alignments)
131.809 Million cell updates/sec

Title: US-09-628-126-8
Perfect score: 1220
Sequence: 1 MDPGLQALNGMAPPGDTAM.....DTSTFPLENLVSLFLYNSD 234

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.AA.*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1220	100.0	234	1 US-08-225-989-8	Sequence 8, Appli
2	1220	100.0	234	1 US-08-570-923-8	Sequence 8, Appli
3	1220	100.0	234	1 US-08-580-014-8	Sequence 8, Appli
4	1220	100.0	234	4 US-09-079-785-8	Sequence 8, Appli
5	1118	91.6	215	1 US-08-225-989-23	Sequence 23, Appli
6	1118	91.6	215	1 US-08-570-923-23	Sequence 23, Appli
7	1118	91.6	215	1 US-08-580-014-23	Sequence 23, Appli
8	1118	91.6	215	4 US-09-079-785-23	Sequence 23, Appli
9	860.5	70.5	239	1 US-08-225-989-6	Sequence 6, Appli
10	860.5	70.5	239	1 US-08-570-923-6	Sequence 6, Appli
11	860.5	70.5	239	1 US-08-580-014-6	Sequence 6, Appli
12	860.5	70.5	239	4 US-09-079-785-6	Sequence 6, Appli
13	814.5	66.8	220	1 US-08-225-989-19	Sequence 19, Appli
14	814.5	66.8	220	1 US-08-570-923-19	Sequence 19, Appli
15	814.5	66.8	220	1 US-08-580-014-19	Sequence 19, Appli
16	814.5	66.8	220	4 US-09-079-785-19	Sequence 19, Appli
17	775	63.5	148	3 US-08-584-031-12	Sequence 12, Appli
18	615	50.4	125	1 US-08-225-989-20	Sequence 20, Appli
19	615	50.4	125	1 US-08-570-923-20	Sequence 20, Appli
20	615	50.4	125	1 US-08-580-014-20	Sequence 20, Appli
21	615	50.4	125	4 US-09-079-785-20	Sequence 20, Appli
22	447.5	36.7	130	1 US-08-225-989-21	Sequence 21, Appli
23	447.5	36.7	130	1 US-08-570-923-21	Sequence 21, Appli
24	447.5	36.7	130	1 US-08-580-014-21	Sequence 21, Appli
25	447.5	36.7	130	4 US-09-079-785-21	Sequence 21, Appli
26	274	22.5	52	4 US-09-369-494-17	Sequence 17, Appli
27	274	22.5	52	4 US-09-358-569D-15	Sequence 15, Appli

28 102 8.4 279 5 PCT-US95-00362-5 Sequence 5, Appli
29 92 7.5 378 3 US-08-630-172-21 Sequence 21, Appli
30 92 7.5 378 4 US-09-375-419-21 Sequence 21, Appli
31 91.5 7.5 376 3 US-08-751-512-8 Sequence 8, Appli
32 90.5 7.4 145 3 US-08-630-172-5 Sequence 5, Appli
33 90.5 7.4 145 4 US-09-375-419-5 Sequence 5, Appli
34 90.5 7.4 179 3 US-08-649-100-9 Sequence 9, Appli
35 90.5 7.4 281 2 US-08-810-453-2 Sequence 2, Appli
36 90.5 7.4 281 3 US-08-815-190A-2 Sequence 2, Appli
37 90.5 7.4 281 4 US-09-290-640-25 Sequence 25, Appli
38 90.5 7.4 281 4 US-09-479-524-3 Sequence 3, Appli
39 90.5 7.4 281 5 PCT-US95-00362-2 Sequence 2, Appli
40 90.5 7.4 287 3 US-08-815-190A-16 Sequence 16, Appli
41 90 7.4 141 4 US-09-286-529-22 Sequence 22, Appli
42 90 7.4 149 3 US-08-584-031-17 Sequence 17, Appli
43 86 7.0 158 1 US-07-994-469A-99 Sequence 99, Appli
44 85.5 7.0 309 1 US-08-236-918A-2 Sequence 2, Appli
45 85 7.0 161 1 US-07-994-469A-61 Sequence 61, Appli

ALIGNMENTS

RESULT 1
US-08-225-989-8
; Sequence 8, Application US/08225989
; Patent No. 5480981
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; APPLICATION DATA:
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-570-923-8

Query Match 100.0%; Score 1220; DB 1; Length 234;
Best Local Similarity 100.0%; Pred. No. 6.4e-125;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MDPLGQALNGMAPPGDTAMHPAGSVASHLGTTSRSYFYLTATLALCLVFTVATIMVL 60

Qy 61 VVQRTDISPNPDVPLKGGNCSEDLICILRAPPKSWAYLQVAKHLNKTLSWNRDGI 120
Db 61 VVQRTDISPNPDVPLKGGNCSEDLICILRAPPKSWAYLQVAKHLNKTLSWNRDGI 120

Qy 121 LHGVRYQDGNLVIFQPGLYFTICQLQFLVQCPNNNSVDIKLELLNKHKKKALVTVCESG 180
Db 121 LHGVRYQDGNLVIFQPGLYFTICQLQFLVQCPNNNSVDIKLELLNKHKKKALVTVCESG 180

Qy 181 MQTKHVYQNLSQLLDYLVQNTTISVNVDTFQYIDTSTFPLENVLSIFLYSNSD 234
Db 181 MQTKHVYQNLSQLLDYLVQNTTISVNVDTFQYIDTSTFPLENVLSIFLYSNSD 234

RESULT 3
US-08-580-014-8
; Sequence 8, Application US/08580014
; Patent No. 5753203
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,014
; FILING DATE: 20-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 22, 2002, 08:16:15 ; Search time 55.1 Seconds
(without alignments)
330.412 Million cell updates/sec

Title: US-09-628-126-6
Perfect score: 1246
Sequence: 1 MEPGLQAGSCGAPSPDPAM.....DTNTPPLDNVLSVFLYSSD 239
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1246	100.0	239	2 B40710	CD30 ligand - mouse
2	860.5	69.1	234	2 A40710	CD30 ligand - human
3	123	9.9	279	2 A53062	Fas ligand - mouse
4	102	8.2	278	2 A49266	Fas ligand - rat
5	91	7.3	309	2 I53384	4-1BB ligand - mouse
6	89.5	7.2	235	2 I54490	tumor necrosis factor
7	89.5	7.2	235	2 S74767	hypothetical protein
8	87	7.0	281	2 I38707	Fas ligand - human
9	87	7.0	2013	2 C71610	probable membrane protein
10	86.5	6.9	2195	2 S61103	SEC16 protein - yeast
11	86	6.9	674	2 S61181	hypothetical protein
12	85.5	6.9	994	2 H96510	probable disease receptor
13	84.5	6.8	884	2 T02731	serine/threonine kinase
14	84	6.7	1110	2 F84547	probable disease receptor
15	83	6.7	889	2 T45691	receptor-like protein
16	82	6.6	234	1 JH0529	tumor necrosis factor
17	82	6.6	665	2 T06082	protein kinase homologue
18	81.5	6.5	304	2 T27593	hypothetical protein
19	81.5	6.5	304	2 T27594	hypothetical protein
20	81	6.5	866	2 T10587	serine/threonine kinase
21	81	6.5	890	2 C96654	hypothetical protein
22	80.5	6.5	344	2 T05104	hypothetical protein
23	80.5	6.5	663	2 H96533	hypothetical protein
24	80	6.4	165	2 H64460	hypothetical protein
25	80	6.4	369	2 S77028	protein kinase, 41 kDa
26	79.5	6.4	383	2 S67813	probable membrane protein
27	79.5	6.4	818	2 T02823	probable membrane protein
28	79.5	6.4	1402	2 T17456	cell surface protein
29	79	6.3	851	2 S67285	NUD1 protein - yeast

30	78.5	6.3	234	1 J01344	tumor necrosis factor
31	78.5	6.3	235	2 J00029	tumor necrosis factor
32	78.5	6.3	960	2 T24221	hypothetical protein
33	78.5	6.3	1150	2 S49956	probable membrane protein
34	78.5	6.3	1706	2 I84499	zinc finger protein
35	78	6.3	395	1 BMH02	bone morphogenetic protein
36	78	6.3	427	2 T40084	hypothetical protein
37	78	6.3	616	2 T32131	hypothetical protein
38	78	6.3	859	1 VCLJMN	env polyprotein nucleocapsid
39	77.5	6.2	463	2 S37962	probable purine nucleoside transferase
40	77.5	6.2	1583	2 S59644	sister chromatid cohesion
41	77	6.2	428	2 T48284	hypothetical protein
42	77	6.2	568	2 T20421	hypothetical protein
43	77	6.2	686	2 F36542	probable protein kinase
44	77	6.2	769	2 T39089	hypothetical protein
45	77	6.2	795	2 H84944	phenylalanine-tRNA synthetase

ALIGNMENTS

RESULT 1
B40710
CD30 ligand - mouse
C:Species: Mus musculus (house mouse)
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999
C:Accession: B40710
R:Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah, T.; Baker, E.; Sutherland, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage, J.; Alderson, M.; Cell 73, 1349-1360, 1993
A:Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de
A:Reference number: A40710; MUID:93313964
A:Accession: B40710
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-239 <SMI>
A:Cross-references: GB:L09754; NID:g349288; PIDN:AAA74595.1; PID:g349289
C:Keywords: cytokine receptor; membrane protein; surface antigen

Query Match 100.0%; Score 1246; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 6.4e-106;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MEPGLQAGSCGAPSPDPAMQVPGSVASPMWRSTSRSYFLSTALVCLVAVVA	60
Qy	61	IILVLVQVKDSTPNTTEKAPLKGNCSEDLFCITLKSTPSKKSWAYLQVSKHLNNTKLSW	120
Db	61	IILVLVQVKDSTPNTTEKAPLKGNCSEDLFCITLKSTPSKKSWAYLQVSKHLNNTKLSW	120
Qy	121	NEDGTIHLIYQDGNLIYVQFGLYFIVCOLQPLVOCNSHNSVDLTQLQLINSIKKQTLVT	180
Db	121	NEDGTIHLIYQDGNLIYVQFGLYFIVCOLQPLVOCNSHNSVDLTQLQLINSIKKQTLVT	180
Qy	181	VCSGVQSKNIYQNLQSFLLHYLQVNSISVRVDNFQYVDTNTPFLDNVLSVFLYSSD	239
Db	181	VCSGVQSKNIYQNLQSFLLHYLQVNSISVRVDNFQYVDTNTPFLDNVLSVFLYSSD	239

RESULT 2

A40710
CD30 ligand - human
C:Species: Homo sapiens (man)
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 21-Jul-2000
C:Accession: A40710
R:Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah, T.; Baker, E.; Sutherland, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage, J.; Alderson, M.; Cell 73, 1349-1360, 1993
A:Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de
A:Reference number: A40710; MUID:93313964
A:Accession: A40710

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 22, 2002, 08:19:35 ; Search time 33.56 Seconds
(without alignments)
261.111 Million cell updates/sec

Title: US-09-628-126-6
Perfect score: 1246
Sequence: 1 MEPLQAGCGSPDPAM.....DTNFTPLDNLVSLYSSSD 239

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Minimum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result #	No.	Score	Query Match %	Length	ID	Description
1	1246	100.0	239	1	TNF8_MOUSE	P32972 mus musculus
2	860.5	69.1	234	1	TNF8_HUMAN	P32971 homo sapien
3	123	9.9	279	1	FASL_MOUSE	P41047 mus musculus
4	102	8.2	278	1	FASL_RAT	P36940 rattus norv
5	91	7.3	309	1	41BL_MOUSE	P41274 mus musculus
6	89.5	7.2	235	1	TNFA_PERLE	P36939 peromyscus
7	87	7.0	281	1	FASL_HUMAN	P48023 homo sapien
8	86.5	6.9	233	1	TNFA_MACMU	P48094 macaca mula
9	86.5	6.9	2194	1	SC16_YEAST	P48415 saccharomyc
10	85	6.8	291	1	TN10_MOUSE	P50592 mus musculus
11	84.5	6.8	525	1	C307_DROME	Q9vrm7 drosophila
12	83.5	6.7	201	1	TNFB_MACEU	Q9xt48 macropus eu
13	83.5	6.7	233	1	TNFA_MACEU	P79337 macaca fasc
14	82.5	6.6	233	1	TNFA_PAPHU	O77510 papio hamad
15	82.5	6.6	965	1	AMPN_MOUSE	P97449 mus musculus
16	82.5	6.6	1078	1	S24A_HUMAN	O95486 homo sapien
17	82	6.6	234	1	TNFA_SHEEP	P33383 ovis aries
18	81.5	6.5	233	1	TNFA_CANEA	P51742 canis famill
19	81	6.5	460	1	ENV_HV123	P12491 human immun
20	80.5	6.5	1376	1	RPOD_ARATH	P56764 arabidopsis
21	79.5	6.4	383	1	COS7_YEAST	Q07788 saccharomyc
22	79	6.3	229	1	TNFA_CEREL	P51743 cervus elap
23	79	6.3	851	1	NUD1_YEAST	P32336 saccharomyc
24	78.5	6.3	234	1	TNFA_HORSE	P29553 equus cabal
25	78.5	6.3	235	1	TNFA_RAT	P16599 rattus norv
26	78.5	6.3	507	1	C392_DROME	P82713 drosophila
27	78.5	6.3	816	1	NEL2_RAT	Q62918 rattus norv
28	78.5	6.3	1150	1	IRR1_YEAST	P40541 saccharomyc
29	78	6.3	396	1	BMP2_HUMAN	P12643 homo sapien
30	78	6.3	856	1	ENV_HV1MN	P05677 human immun
31	77.5	6.2	178	1	IL10_MACFA	P79338 macaca fasc
32	77.5	6.2	463	1	YRN3_YEAST	P36066 saccharomyc
33	77.5	6.2	1583	1	MIS4_SCHPO	Q09725 schizosacch

ALIGNMENTS

RESULT 1
TNF8_MOUSE STANDARD; PRT; 239 AA.
AC P32972;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CD30 LIGAND (CD30-L).
GN TNFSF8 OR CD30LG OR CD30L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=93313964; PubMed=8391931;
RA Smith C.A., Gruess H.-J., Davis T., Anderson D., Parrah T.,
RA Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA Grabstein K.H., Gliniak B., McAlister I.B., Fanslow W., Alderson M.,
RA Falk B., Gimpel S., Gillis S., Din W.S., Goodwin R.G., Armitage R.J.;
RT "CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose
RT ligand defines an emerging family of cytokines with homology to
RT TNF.";
RL Cell 73:1349-1360(1993).
CC -!- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF
CC T CELLS.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L09754; AAA74595.1; -
CC PIR: B40710; B40710.
CC MGD: MGI:88328; Tnf8.
CC InterPro: IPR003638; TNF_8.
CC InterPro: IPR000478; TNF_family.
CC Pfam: PF00229; TNF; 1.
CC ProDom: PD023087; TNF_8; 1.
CC SMART: SM00207; TNF; 1.
CC PROSITE: PS00251; TNF_1; 1.
CC PROSITE: PSS00049; TNF_2; 1.
CC Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
CC DOMAIN 1 43
CC CYTOPLASMIC (POTENTIAL).
CC SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
CC TRANSMEM 44 67
CC EXTRACELLULAR (POTENTIAL).
CC DOMAIN 68 239
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 75 75
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 86 86
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 114 114
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 158 158
CC FT CARBOHYD

34 77 6.2 795 1 SYFB_BUCAI P57230 buchnera ap
35 76.5 6.1 317 1 TN11_HUMAN O14788 h tumor nec
36 76.5 6.1 345 1 OPCM_BOVIN P11834 bos taurus
37 76.5 6.1 1073 1 HSER_PIG P5204 sus scrofa
38 76 6.1 234 1 TNFA_CAVPO P51435 cavia porce
39 76 6.1 520 1 C4P2_DROME Q9V557 drosophila
40 75.5 6.1 178 1 IL10_CERTO P46651 cercocebus
41 75.5 6.1 383 1 COS5_YEAST P47187 saccharomyc
42 75.5 6.1 1178 1 PH81_YEAST P17442 saccharomyc
43 75 6.0 179 1 I10H_HSYE2 Q89451 equine herp
44 75 6.0 524 1 2A5G_HUMAN Q13362 h serine/th
45 75 6.0 524 1 2A5G_RABIT Q28651 o serine/th

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FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 239 AA; 26519 MW; 29003157DD425159 CRC64;

Query Match 100.0%; Score 1246; DB 1; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.1e-107;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPGLQAGSCGAPSPDPAMQVPGSVASVSPWRSTRPWRSTRSYFYLLSTTALVCLVAVVA 60
Db 1 MEPGLQAGSCGAPSPDPAMQVPGSVASVSPWRSTRPWRSTRSYFYLLSTTALVCLVAVVA 60

QY 61 IILVIVVOKKDSPTNTTEKAPLKGNCSEDLFCTLKSTPSKKSWAYLOVSKHLNNTKLSW 120
Db 61 IILVIVVOKKDSPTNTTEKAPLKGNCSEDLFCTLKSTPSKKSWAYLOVSKHLNNTKLSW 120

QY 121 NEDGTHGLIYQDGNLIVQFPGLYFIVCOLQFLVQCNSHNSVDLTQLLLINSKIKKQTLV 180
Db 121 NEDGTHGLIYQDGNLIVQFPGLYFIVCOLQFLVQCNSHNSVDLTQLLLINSKIKKQTLV 180

QY 181 VCESGVQSKNIYQNLSQFLHLYLQVNSTISVRVDNFQYVDNTFPPLDNVLSVFLYSSSD 239
Db 181 VCESGVQSKNIYQNLSQFLHLYLQVNSTISVRVDNFQYVDNTFPPLDNVLSVFLYSSSD 239

RESULT 2
TNF8_HUMAN STANDARD; PRT; 234 AA.
AC P32971;
DT 01-OCT-1993 (Rel. 27, Created).
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CD30 LIGAND (CD30-L) (CD153 ANTIGEN).
GN TNFSF8 OR CD30LG OR CD30L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93313964; PubMed=8301931;
RA Smith C.A., Gruess H.-J., Davis T., Anderson D., Farrah T.,
RA Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA Grabstein K.H., Gliniak B., McAlister I.B., Fanslow W., Alderson M.,
RA Falk B., Gimpel S., Gillis S., Din W.S., Goodwin R.G., Armitage R.J.;
RA "CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose
RA ligand defines an emerging family of cytokines with homology to
RA TNF."
RL Cell 73:1349-1360(1993).
CC -!- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF
CC T CELLS.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD153 entry.
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd153.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
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DR PROSITE; PS00251; TNF-1; 1.
DR PROSITE; PS50049; TNF-2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 62 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 63 234 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 234 AA; 26017 MW; C653615682305B1B CRC64;

Query Match 69.1%; Score 860.5; DB 1; Length 234;
Best Local Similarity 69.6%; Pred. No. 8.6e-72;
Matches 167; Conservative 28; Mismatches 38; Indels 7; Gaps 2;

QY 1 MEPGLQAGSCGAPSPDPAMQVPGSVASVSPWRSTRPWRSTRSYFYLLSTTAL-VCLVAVV 59
Db 1 MDPGLQALNGMAPPGDTAMHVPAGSVAS-----HLGTTSTRSYFYLLTATLALCLVFTV 54

QY 60 AILVIVVOKKDSPTNTTEKAPLKGNCSEDLFCTLKSTPSKKSWAYLOVSKHLNNTKLS 119
Db 55 ATIMVIVVORTDSTIPNSPDNVPKGCNSEDLLICLRAPFRKRSWAYLOVAKHLNNTKLS 114

QY 120 WNEDGTHGLIYQDGNLIVQFPGLYFIVCOLQFLVQCNSHNSVDLTQLLLINSKIKKQTLV 179
Db 115 WNKDGLHGVRYQDGNLIVQFPGLYFIIICQLQFLVQCPNNSVDLLELLINKHKQALV 174

QY 180 TVCESGVQSKNIYQNLSQFLHLYLQVNSTISVRVDNFQYVDNTFPPLDNVLSVFLYSSSD 239
Db 175 TVCESGMQTKHYQNLSQFLLDLYLVQNTTISVNVDTFQYIDTSTFPLENVLSIFLYSNSD 234

RESULT 3
FASL_MOUSE STANDARD; PRT; 279 AA.
AC P41047; Q61217; Q9R1F2;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE FAS ANTIGEN LIGAND.
GN TNFSF6 OR APTLIG1 OR FASL OR GLD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=94185175; PubMed=7511063;
RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
RA Suda T., Nagata S.;
RA "Generalized lymphoproliferative disease in mice, caused by a point
RA mutation in the Fas ligand.";
RL Cell 76:969-976(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.
RC STRAIN=C57BL/6;
RX MEDLINE=95388076; PubMed=7544870;
RA Peitsch M.J., Tschoep J.J.;
RA "Comparative molecular modelling of the Fas-ligand and other members
RA of the TNF family.";
RL Mol. Immunol. 32:761-772(1995).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=95196085; PubMed=7889405;
RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
RA "The mouse Fas-ligand gene is mutated in gid mice and is part of a
RA TNF family gene cluster.";
RL Immunity 1:131-136(1994).
RN [4]
```

GenCore version 4.5
 Copyright (c) 1993 - 2000 CompuGen Ltd.
 OM protein - protein search, using sw model
 Run on: January 22, 2002, 08:17:50 ; Search time 96.97 Seconds
 (without alignments)
 360.514 Million cell updates/sec

Title: US-09-628-126-6
 Perfect score: 1246
 Sequence: 1 MEPLQAGSCGAPSPDPAM.....DTNTPFLDNVLSVFLYSSSD 239

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_17:

- 1: sp-archaea:*
- 2: sp-bacteria:*
- 3: sp-fungi:*
- 4: sp-human:*
- 5: sp-invertebrate:*
- 6: sp-mammal:*
- 7: sp-mhc:*
- 8: sp-organelle:*
- 9: sp-phage:*
- 10: sp-plant:*
- 11: sp-rodent:*
- 12: sp-virus:*
- 13: sp-vertebrate:*
- 14: sp_unclassified:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	840.5	67.5	234	043404	Q43404 homo sapien
2	90.5	7.3	797	12 Q99BY2	Q99BY2 human immun
3	90	7.2	280	6 Q9WLF6	Q9WLF6 macaca neme
4	89.5	7.2	225	13 Q9IB42	Q9IB42 paralichthy
5	89.5	7.2	401	2 P72902	P72902 synechocyst
6	89.5	7.2	847	12 Q9WIS1	Q9WIS1 human immun
7	89	7.1	169	11 Q9WV90	Q9WV90 marmota mon
8	88	7.1	234	6 Q28320	Q28320 capra hircu
9	87.5	7.0	896	10 Q9M9H0	Q9M9H0 arabiidopsis
10	87	7.0	858	12 Q99C07	Q99C07 human immun
11	87	7.0	2013	5 Q96216	Q96216 plasmodium
12	86.5	6.9	217	11 Q9ERG6	Q9ERG6 peromyscus
13	86.5	6.9	280	6 Q9BDN1	Q9BDN1 cercocobus
14	86.5	6.9	280	6 Q9EDM5	Q9EDM5 macaca mula
15	86.5	6.9	579	4 Q9BY79	Q9BY79 homo sapien
16	86.5	6.9	2195	3 Q02822	Q02822 saccharomyc
17	86	6.9	674	3 Q06629	Q06629 saccharomyc
18	85.5	6.9	282	6 Q9BEA8	Q9BEA8 sus scrofa
19	85.5	6.9	873	10 Q9FID8	Q9FID8 arabiidopsis

20	85.5	6.9	994	10 Q9C637	Q9C637 arabiidopsis
21	85	6.8	283	10 Q9FKU2	Q9FKU2 arabiidopsis
22	85	6.8	699	12 Q9DPZ6	Q9DPZ6 human immun
23	85	6.8	852	12 Q99BZ7	Q99BZ7 human immun
24	84.5	6.8	208	2 O68241	O68241 pantoea cit
25	84.5	6.8	884	10 O81069	O81069 arabiidopsis
26	84	6.7	282	12 Q9IC83	Q9IC83 kaposi's sa
27	84	6.7	424	11 Q9DC72	Q9DC72 mus musculu
28	84	6.7	537	13 Q98ST8	Q98ST8 brachydanio
29	84	6.7	544	12 Q64940	Q64940 avian infec
30	84	6.7	1110	10 Q9SDA5	Q9SDA5 arabiidopsis
31	83	6.7	889	10 Q9SNA3	Q9SNA3 arabiidopsis
32	82.5	6.6	966	11 Q99K63	Q99K63 mus musculu
33	82.5	6.6	1328	4 Q9POV5	Q9POV5 homo sapien
34	82	6.6	665	10 Q9T0J1	Q9T0J1 arabiidopsis
35	81.5	6.5	151	5 Q9GP20	Q9GP20 globodera r
36	81.5	6.5	304	5 Q94382	Q94382 caenorhabdi
37	81.5	6.5	304	5 Q94383	Q94383 caenorhabdi
38	81	6.5	745	2 Q9K5C7	Q9K5C7 claviibacter
39	81	6.5	866	10 Q9SUN4	Q9SUN4 arabiidopsis
40	81	6.5	890	10 Q91Q11	Q91Q11 arabiidopsis
41	81	6.5	1391	12 Q9DPK7	Q9DPK7 meleagrid h
42	81	6.5	1409	12 Q9ELH3	Q9ELH3 meleagrid h
43	80.5	6.5	216	6 Q9BEC4	Q9BEC4 talpa europ
44	80.5	6.5	344	10 O81781	O81781 arabiidopsis
45	80.5	6.5	663	10 Q9FX99	Q9FX99 arabiidopsis

ALIGNMENTS

RESULT 1
 043404 ID 043404 PRELIMINARY; PRT; 234 AA.
 AC 043404;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CD30L PROTEIN.
 GN CD30L.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98007874; PubMed=9349718;
 RA Croager E.J., Abraham L.J.;
 RT "Characterisation of the human CD30 ligand gene structure.";
 RL Biochim. Biophys. Acta 1353:231-235(1997).
 DR EMBL; AF006384; AAB97877.1;
 DR EMBL; AF006381; AAB97877.1; JOINED.
 DR EMBL; AF006382; AAB97877.1; JOINED.
 DR EMBL; AF006383; AAB97877.1; JOINED.
 DR InterPro; IPR000478; TNF family.
 DR InterPro; IPR003638; TNF_8.
 DR Pfam; PF00229; TNF_1.
 DR ProDom; PD023087; TNF_8; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS50049; TNF_2; 1.
 DR SMART; SM00207; TNF; 1.
 SQ SEQUENCE 234 AA; 25963 MW; 37BA5733C7911751 CRC64;

Query Match 67.5%; Score 840.5; DB 4; Length 234;
 Best Local Similarity 68.3%; Pred. No. 3.4e-72;
 Matches 164; Conservative 28; Mismatches 41; Indels 7; Gaps 2;

QY 1 MEPLQAGSCGAPSPDPAMQVQPGSVASPRWRTRPWRSTSRFSYLTAL-VCLVAV 59
 Db 1 MDPGLQALNGMAPPGDTAMHVPAGSVAS-----HLGTTSRSYFLATLALCLVFTV 54
 QY 60 AIIILVIVQKDKDTPNTEKAPLKGNCSEDLFCTLKSTPSKKWAYLQVSKHLNNTKLS 119

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Db 55 ATTWLVVQRTSDIPNSPDWVPLKGGNCSEDLJCILRAPFKKSWAYLQVAKHLNKTLS 114
Qy 120 WNEGDTHGLIYQDGNLIVQPGGLYFTVQCLQFLVQCSNHSVDLTQLLINSKIKKQTLV 179
Db 115 WNKDGLHGVYQDGNLIVQPGGLYFTVQCLQFLVQCPNNSVDLKKXELLINKHKQXLV 174
Qy 180 TVCESGVQSKNIYQNLISQFLHLYQVNSTISVRVDNFQYVDNTFFLDNLVLSVFLYSSD 239
Db 175 TVCESGMQTKHYQNLISQFLLDYQVNSTISVNVDTQYIDTSTFFLENVLSIELXNSD 234

RESULT 2
Q99BY2 ID Q99BY2 PRELIMINARY; PRT; 797 AA.
AC Q99BY2;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RA Sutherland R., Srisurapanon S.;
RT "Biological and immunological characteristics of HIV-1 subtype E in cerebrospinal fluid and blood.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF322200; AAK09407.1; -.
FT NON-TER 797
FT NON-TER 797
SQ SEQUENCE 797 AA; 90476 MW; 1C192A1DE05992C2 CRC64;
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Query Match 7.3%; Score 90.5; DB 12; Length 797;
Best Local Similarity 22.5%; Pred. No. 2.6;
Matches 43; Conservative 36; Mismatches 59; Indels 53; Gaps 11;

Qy 59 VAILVLVQKDKSTNTTEKAPLKGNCSEDL-FCTLKST---PSKKSWAY-----LQV 109
Db 72 LCVTLKCTEAKLNKNTTNTND-PIKIGNLTDEVRNCSFKMTTELKDKKQVYALFYKLDI 130
Qy 110 SKHLNNTKLSWNEGDTHGLIYQDGNLIVQ-----PGLYFIV----- 147
Db 131 VPIKENNRSYSE-----YRLINCNTSVIKQACPKISFDPIPIHYCTPAGYAILKCNKNF 186
Qy 148 -----COIQFLVQCSNHSVD--LTQLLLINSKIKKQTLVTVCESGVQSKNIYQNLISQFL 200
Db 187 NGTGPKCKNVSSVQCT-HGIKPVVTTQLLNGSLAEIEII-----IRSENLTNNAKNIIV 239
Qy 201 HY---LQVNST 208
Db 240 HLKNSVEINCT 250
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RESULT 3
Q9MYL6 ID Q9MYL6 PRELIMINARY; PRT; 280 AA.
AC Q9MYL6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE FAS LIGAND.
GN PT-FASL OR CM-FASL OR RM-FASL.
OS Macaca nemestrina (Pig-Tailed macaque),
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9545, 9541, 9544;
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RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.nemestrina; STRAIN=PIG-TAILED MONKEY;
RA Kirii Y., Inoue T., Yoshino K.;
RT "Pig-tailed monkey Fas ligand mRNA, complete cds.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.fascicularis; STRAIN=CYNOMOLGUS MONKEY;
RA Kirii Y., Inoue T., Yoshino K.;
RT "Cynomolgus monkey Fas ligand mRNA, complete cds.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
[3]
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta; STRAIN=RHEBUS MONKEY;
RA Kirii Y., Inoue T., Yoshino K.;
RT "Rhesus monkey Fas ligand mRNA, complete cds.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB035140; BAA90296.1; -.
DR EMBL; AB035138; BAA90294.1; -.
DR EMBL; AB035139; BAA90295.1; -.
DR InterPro; IPR003263; TNF_5.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNCRSISFCT.
DR PRODOM; PD008600; TNF_5; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
SQ SEQUENCE 280 AA; 31367 MW; F0B284D61A132EB4 CRC64;

Query Match 7.2%; Score 90; DB 6; Length 280;
Best Local Similarity 21.1%; Pred. No. 0.96;
Matches 52; Conservative 37; Mismatches 75; Indels 82; Gaps 12;

Qy 14 PSPDPAMQVQPGSVASPMWRSTRPMRSTRSFYLTALVCLVAVAIILVLVY----- 67
Db 59 PSLPLPLPLPP-----LKRGNHSTG-----LCLLVMFVVALVGLGLGM 100
Qy 68 -----QKDKSTPNTTEKAPLKGNCSEDLFCTLKS-----TPSKKSW---AYLQVSK 111
Db 101 FQLFHLQK-----ELAEELRESTSQKHTASSLEKQIGHPSPPPEKQKQVHLTGKP 152
Qy 112 HLNNTKLSWNEGDTHGLIYQDGNLIVQPGGLYFIVQCLQFLVQ-CSN-----HSVDL 163
Db 153 NSRSMPLWEDTYGLVLLSGVAKKGLVNETGLYFYYSKYFRGQSCNTNPLSHKV-- 210
Qy 164 TLOLLINSK-----IKKQTLVTVCEG-----VQSKNIYQNLISQFLHY 202
Db 211 ---YMRNSKYPQDLVMMESKMSYCTTGQMAHSSYLGAVFNLTSADHLVYVNVSELSVN 267
Qy 203 LQVNST 208
Db 268 FEESQT 273

RESULT 4
Q9IB42 ID Q9IB42 PRELIMINARY; PRT; 225 AA.
AC Q9IB42;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR.
GN OS Paracithys olivaceus (Flounder).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Bothidae; Paracithys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 22, 2002, 08:16:15 ; Search time 39.95 Seconds
(without alignments)
134.625 Million cell updates/sec

Title: US-09-628-126-6
Perfect score: 1246
Sequence: 1 MEPLQAGSCGAPSPDPAM.....DTNFTPLDNLVFLYSSD 239

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	% Match	Query Length	DB ID	Description
1	1246	100.0	239	1	US-08-225-989-6 Sequence 6, Appl
2	1246	100.0	239	1	US-08-570-923-6 Sequence 6, Appl
3	1246	100.0	239	1	US-08-580-014-6 Sequence 6, Appl
4	1246	100.0	239	1	US-09-079-785-6 Sequence 6, Appl
5	1141	91.6	220	1	US-08-225-989-19 Sequence 19, Appl
6	1141	91.6	220	1	US-08-570-923-19 Sequence 19, Appl
7	1141	91.6	220	1	US-08-580-014-19 Sequence 19, Appl
8	1141	91.6	220	1	US-09-079-785-19 Sequence 19, Appl
9	860.5	69.1	234	1	US-08-225-989-8 Sequence 8, Appl
10	860.5	69.1	234	1	US-08-570-923-8 Sequence 8, Appl
11	860.5	69.1	234	1	US-08-580-014-8 Sequence 8, Appl
12	860.5	69.1	234	1	US-09-079-785-8 Sequence 8, Appl
13	814.5	65.4	215	1	US-08-225-989-23 Sequence 23, Appl
14	814.5	65.4	215	1	US-08-570-923-23 Sequence 23, Appl
15	814.5	65.4	215	1	US-08-580-014-23 Sequence 23, Appl
16	814.5	65.4	215	4	US-09-079-785-23 Sequence 23, Appl
17	685	55.0	130	1	US-08-225-989-21 Sequence 21, Appl
18	685	55.0	130	1	US-08-570-923-21 Sequence 21, Appl
19	685	55.0	130	1	US-08-580-014-21 Sequence 21, Appl
20	685	55.0	130	1	US-09-079-785-21 Sequence 21, Appl
21	624	50.1	148	3	US-08-584-031-12 Sequence 12, Appl
22	391.5	31.4	125	1	US-08-225-989-20 Sequence 20, Appl
23	391.5	31.4	125	1	US-08-570-923-20 Sequence 20, Appl
24	391.5	31.4	125	1	US-08-580-014-20 Sequence 20, Appl
25	391.5	31.4	125	4	US-09-079-785-20 Sequence 20, Appl
26	229	18.4	52	4	US-09-369-494-17 Sequence 17, Appl
27	229	18.4	52	4	US-09-358-569D-15 Sequence 15, Appl

28 115 9.2 279 5 PCT-US95-00362-5 Sequence 5, Appl
29 91 7.3 309 1 US-08-236-918A-2 Sequence 2, Appl
30 87 7.0 281 2 US-08-810-453-2 Sequence 2, Appl
31 87 7.0 281 3 US-08-815-190A-2 Sequence 2, Appl
32 87 7.0 281 4 US-09-290-640-25 Sequence 25, Appl
33 87 7.0 281 4 US-09-479-524-3 Sequence 3, Appl
34 87 7.0 281 5 PCT-US95-00362-2 Sequence 2, Appl
35 85 6.8 291 1 US-08-670-354-6 Sequence 6, Appl
36 85 6.8 291 4 US-09-320-424-6 Sequence 6, Appl
37 85 6.8 291 5 PCT-US96-10895-6 Sequence 6, Appl
38 83 5 6.7 287 3 US-08-815-190A-16 Sequence 16, Appl
39 83 6.7 550 2 US-08-417-210A-140 Sequence 140, App
40 83 6.7 551 2 US-08-417-210A-137 Sequence 137, App
41 83 6.7 551 2 US-08-417-210A-143 Sequence 143, App
42 83 6.7 857 1 US-08-022-835-4 Sequence 4, Appl
43 83 6.7 857 1 US-08-388-809-4 Sequence 4, Appl
44 83 6.7 857 2 US-08-647-714-4 Sequence 4, Appl
45 82.5 6.6 183 4 US-09-105-343A-8 Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-225-989-6
; Sequence 6, Application US/08225989
; Patent No. 5480981
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644

TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-225-989-6

Query Match 100.0%; Score 1246; DB 1; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.3e-116;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEPGLQAGSCGAPSPDPAMQVPGSVASVSPWRSTRPWRSTRSYFYLTALVCLVAVVA 60
Db 1 MEPGLQAGSCGAPSPDPAMQVPGSVASVSPWRSTRPWRSTRSYFYLTALVCLVAVVA 60
QY 61 IILVLVVKKDSPTNTEKAPLKGNCSEDLFCTLKSTPSKSKSWAYLQVSKHLNNTKLSW 120
Db 61 IILVLVVKKDSPTNTEKAPLKGNCSEDLFCTLKSTPSKSKSWAYLQVSKHLNNTKLSW 120
QY 121 NEDGTIHLIYQDGNLIYQFPGLYFIVCQLQFLVQCSNHSVDLTQLLLINSKIKKQTLVT 180
Db 121 NEDGTIHLIYQDGNLIYQFPGLYFIVCQLQFLVQCSNHSVDLTQLLLINSKIKKQTLVT 180
QY 181 VCESGVOSKNIYQNLQSLQFLHYLVQNSTISVRVDFQYVDTNTPFLDNVLSVFLYSSSD 239
Db 181 VCESGVOSKNIYQNLQSLQFLHYLVQNSTISVRVDFQYVDTNTPFLDNVLSVFLYSSSD 239

* RESULT 2

US-08-570-923-6
; Sequence 6, Application US/08570923
; Patent No. 5677430
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,923
; FILING DATE: 12-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-570-923-6

Query Match 100.0%; Score 1246; DB 1; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.3e-116;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEPGLQAGSCGAPSPDPAMQVPGSVASVSPWRSTRPWRSTRSYFYLTALVCLVAVVA 60
Db 1 MEPGLQAGSCGAPSPDPAMQVPGSVASVSPWRSTRPWRSTRSYFYLTALVCLVAVVA 60
QY 61 IILVLVVKKDSPTNTEKAPLKGNCSEDLFCTLKSTPSKSKSWAYLQVSKHLNNTKLSW 120
Db 61 IILVLVVKKDSPTNTEKAPLKGNCSEDLFCTLKSTPSKSKSWAYLQVSKHLNNTKLSW 120
QY 121 NEDGTIHLIYQDGNLIYQFPGLYFIVCQLQFLVQCSNHSVDLTQLLLINSKIKKQTLVT 180
Db 121 NEDGTIHLIYQDGNLIYQFPGLYFIVCQLQFLVQCSNHSVDLTQLLLINSKIKKQTLVT 180
QY 181 VCESGVOSKNIYQNLQSLQFLHYLVQNSTISVRVDFQYVDTNTPFLDNVLSVFLYSSSD 239
Db 181 VCESGVOSKNIYQNLQSLQFLHYLVQNSTISVRVDFQYVDTNTPFLDNVLSVFLYSSSD 239

RESULT 3

US-08-580-014-6
; Sequence 6, Application US/08580014
; Patent No. 5753203
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,014
; FILING DATE: 20-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 22, 2002, 08:17:45 ; Search time 55.1 seconds
(without alignments)
304.145 Million cell updates/sec

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US-09-628-126-19
1141
Title:
Perfect score:
Sequence: 1 MQVPGSVASPWRTRPWRS.....DTNTPLDNLVSLYLYSSD 220
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

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Minimum DB seq length: 0
Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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Database : PIR_68:**
1: pir1:**
2: pir2:**
3: pir3:**
4: pir4:**
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1141	100.0	239	2	B40710	CD30 ligand - mouse
2	814.5	71.4	234	2	A40710	CD30 ligand - human
3	109	9.6	279	2	A53062	Fas ligand - mouse
4	91	8.0	278	2	A49265	Fas ligand - rat
5	89.5	7.8	401	2	S47467	hypothetical protein
6	88.5	7.8	309	2	I53384	hypothetical protein
7	87.5	7.7	235	2	I54490	tumor necrosis factor
8	87	7.6	2013	2	C71610	4-1BB ligand - mouse
9	86.5	7.6	2195	2	S61103	probable membrane protein
10	86	7.5	674	2	S61181	SEC16 protein - yeast
11	85.5	7.5	994	2	H96510	hypothetical protein
12	84.5	7.4	884	2	I02731	probable disease related
13	84	7.4	281	2	I38707	serine/threonine-specific
14	84	7.4	1110	2	F84547	Fas ligand - human
15	82	7.2	234	1	JH0529	probable disease related
16	81.5	7.1	304	2	T27593	tumor necrosis factor
17	81.5	7.1	304	2	T27594	hypothetical protein
18	81	7.1	866	2	T10587	hypothetical protein
19	80.5	7.1	344	2	T05104	serine/threonine-specific
20	80	7.0	165	2	H64460	hypothetical protein
21	80	7.0	369	2	S77028	hypothetical protein
22	79.5	7.0	889	2	T45691	protein kinase, 41 kDa
23	79	6.9	851	2	S67285	receptor-like protein
24	78.5	6.9	924	1	J01344	NUPI protein - yeast
25	78.5	6.9	235	2	JU0029	tumor necrosis factor
26	78.5	6.9	1150	2	S49956	tumor necrosis factor
27	78	6.8	427	2	T40064	probable membrane protein
28	78	6.8	616	2	T32131	hypothetical protein
29	78	6.8	859	1	VCLJMN	env polyprotein precursor

ALIGNMENTS

RESULT 1
B40710
CD30 ligand - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-May-1994 #sequence_revision 03-May-1999 #text_change 05-Nov-1999
C:Accession: B40710
R:Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah, T.; Baker, E.; Sutherland
Aldererson, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage,
Cell 73, 1349-1360, 1993
A:Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de
A:Reference number: A40710; MUID:93313964
A:Accession: B40710
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-239 <SMI>
A:Cross-references: GB:L09754; NID:g349288; PIDN:AAA74595.1; PID:g349289
C:Keywords: cytokine receptor; membrane protein; surface antigen

```
Query Match      100.0%; Score 1141; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.8e-96;
Matches 220: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	MQVPGSVASPWSTRPWRSTRSYFYLSTTALVCLVAVAILVLVQKQKOSTPNTTEK	60
Db	20	MQVPGSVASPWSTRPWRSTRSYFYLSTTALVCLVAVAILVLVQKQKOSTPNTTEK	79
Qy	61	APLKGNCSEDLFCTLKSTPSKSWAYLOVSKHLNNTKLS ⁴ TS ² CT ¹ HGLIYODGNLIVQ	120
Db	80	APLKGNCSEDLFCTLKSTPSKSWAYLOVSKHLNNTKLSWNE ² DGTHGLIYODGNLIVQ	139
Qy	121	FPGLYFTVCLQQLFVOC ² SNHSVDLT ¹ LQLLINSIKKOTLVTVCE ² SGVSKNIYQNL ¹ SQFL	180
Db	140	FPGLYFTVCLQQLFVOC ² SNHSVDLT ¹ LQLLINSIKKOTLVTVCE ² SGVSKNIYQNL ¹ SQFL	199
Qy	181	LHYLVQNSTISVRDNFQYVDTNTFP ¹ LDNVL ¹ SVFLYSSD	220
Db	200	LHYLVQNSTISVRDNFQYVDTNTFP ¹ LDNVL ¹ SVFLYSSD	239

RESULT 2
A40710
CD30 ligand - human
C:Species: Homo sapiens (man)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 21-Jul-2000
C:Accession: A40710
R:Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah, T.; Baker, E.; Sutherland, A.;
Aliderson, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage,
Cell 73, 1349-1360, 1993
A:Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de
A:Reference number: A40710; MUID:93313964
A:Accession: A40710

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OM protein - protein search, using sw model

Run on: January 22, 2002, 08:31:35 ; Search time 33.56 Seconds
(without alignments)
240.353 Million cell updates/sec

Title: US-09-628-126-19

Perfect score: 1141

Sequence: 1 MQVQGSVSPWRTRPWS.....DTNTPLDNLVSLYSSD 220

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1141	100.0	239	1 TNF8_MOUSE	P32972 mus musculus
2	814.5	71.4	234	1 TNF8_HUMAN	P32971 homo sapien
3	109	9.6	279	1 FASL_MOUSE	P41047 mus musculus
4	91	8.0	278	1 FASL_RAT	P36940 rattus norv
5	88.5	7.8	309	1 41BL_MOUSE	P41274 mus musculus
6	87.5	7.7	235	1 TNFA_PERLE	P36939 peromyscus
7	86.5	7.6	2194	1 SC16_YEAST	P48415 saccharomyc
8	85	7.4	291	1 TN10_MOUSE	P50592 mus musculus
9	84.5	7.4	233	1 TNFA_MACMU	P48094 macaca mula
10	84.5	7.4	525	1 C307_DROME	Q9vrm7 drosophila
11	84	7.4	281	1 FASL_HUMAN	P48023 homo sapien
12	83.5	7.3	201	1 TNFB_WACEU	Q9xt48 macropus eu
13	82.5	7.2	965	1 AMFN_MOUSE	P97449 mus musculus
14	82	7.2	234	1 TNFA_SHEEP	P23383 ovis aries
15	81.5	7.1	233	1 TNFA_CANFA	P51742 canis famil
16	81.5	7.1	233	1 TNFA_MACFA	P79337 macaca fasc
17	81	7.1	460	1 ENV_HV123	P12491 human immun
18	80.5	7.1	233	1 TNFA_FAPHU	O77510 papio hamad
19	80	7.0	1376	1 RPOD_ARATH	P56764 arabidopsis
20	79	6.9	229	1 TNFA_CEREL	P51743 cervus elap
21	79	6.9	851	1 NUD1_YEAST	P23336 saccharomyc
22	78.5	6.9	234	1 TNFA_HORSE	P29553 equus cabal
23	78.5	6.9	235	1 TNFA_RAT	P16599 rattus norv
24	78.5	6.9	1150	1 IRR1_YEAST	P40541 saccharomyc
25	78	6.8	856	1 ENV_HV1MN	P05877 human immun
26	77.5	6.8	178	1 IL10_MACFA	P79338 macaca fasc
27	77.5	6.8	463	1 YKN3_YEAST	P36066 saccharomyc
28	77.5	6.8	1583	1 MISA_SCHPO	Q09725 schizosacch
29	77	6.7	795	1 SYFB_BUCAI	P57230 buchnera ap
30	76.5	6.7	317	1 TN11_HUMAN	O14788 h tumor nec
31	76.5	6.7	345	1 OPCM_BOVIN	P11834 bos taurus
32	76.5	6.7	507	1 C392_DROME	P82713 drosophila
33	76.5	6.7	1073	1 HSER_PIG	P55204 sus scrofa

ALIGNMENTS

RESULT 1

ID	TNF8_MOUSE	STANDARD;	PRT;	239 AA.
AC	P32972;			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-OCT-1993 (Rel. 27, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	CD30 LIGAND (CD30-L).			
GN	TNFSF8 OR CD30LG OR CD30L.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
[]				
RN	SEQUENCE FROM N.A.			
RP	TISSUE=T-cell;			
RC	MEDLINE=3313964; PubMed=8391931;			
RA	Smith C.A., Gruess H.-J., Davis T., Anderson D., Farrah T.,			
RA	Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,			
RA	Grabstein K.H., Gliniak B., McAllister I.B., Fanslow W., Alderson M.,			
RA	Falk B., Gimpel S., Gillis S., Din W.S., Goodwin R.G., Armitage R.J.,			
RT	"CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose			
RT	ligand defines an emerging family of cytokines with homology to			
RT	TNF."			
RL	Cell 73:1349-1360(1993).			
CC	-1- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF			
CC	T CELLS.			
CC	-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (CC			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
CC	EMBL: L09754; AAA74595.1; -			
DR	PIR: B40710; B40710.			
DR	MGI: 88328; Tnfsf8.			
DR	InterPro: IPR003638; TNF_8.			
DR	InterPro: IPR000478; TNF_family.			
DR	Pfam: PF00229; TNF; 1.			
DR	ProDom: PD023087; TNF_8; 1.			
DR	SMART: SM00207; TNF; 1.			
DR	PROSITE: PS00251; TNF_1; 1.			
DR	PROSITE: PSS0049; TNF_2; 1.			
DR	Cytokine; Transmembrane; Glycoprotein; Signal-anchor.			
FT	DOMAIN 1 43			
FT	TRANSMEM 44 67			
FT	DOMAIN 68 239			
FT	CARBOHYD 75 75			
FT	CARBOHYD 86 86			
FT	CARBOHYD 114 114			
FT	CARBOHYD 158 158			
FT	CARBOHYD 158 158			

SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
CYTOPLASMIC (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 239 AA; 26519 MW; 29003157DD425159 CRC64;

Query Match 100.0%; Score 1141; DB 1; Length 239;
Best Local Similarity 100.0%; Pred. No. 4.6e-97;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQVQGSVASPRSTRPWRSTSRYSFYLSSTALVCLVAVAILLVVQVKDSTPNTTEK 60
Db 20 MQVQGSVASPRSTRPWRSTSRYSFYLSSTALVCLVAVAILLVVQVKDSTPNTTEK 79

Qy 61 APLKGGNCSEDLCTLKSTPSKSWAYLVQSKHLNNTKLSWNEGTTHGLIYQDGNLIVQ 120
Db 80 APLKGGNCSEDLCTLKSTPSKSWAYLVQSKHLNNTKLSWNEGTTHGLIYQDGNLIVQ 139

Qy 121 FPGLYFYVCOQLQFLVQCSNHSVDLTQLLINSKIKKOTLVTVCSGVQSKNIYQNLSQL 180
Db 140 FPGLYFYVCOQLQFLVQCSNHSVDLTQLLINSKIKKOTLVTVCSGVQSKNIYQNLSQL 199

Qy 181 LHYLVNSTISVRVDFNYVDNTFPDLNLSVFLYSSSD 220
Db 200 LHYLVNSTISVRVDFNYVDNTFPDLNLSVFLYSSSD 239

RESULT 2
TNF8_HUMAN
ID TNF8_HUMAN STANDARD; PRT; 234 AA.
AC P32971;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE CD30 LIGAND (CD30-L) (CD153 ANTIGEN).
-GN TNFSF8 OR CD30LG OR CD30L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
MEDLINE=93313964; PubMed=8391931;
RA Smith C.A., Gruess H.-J., Davis T., Anderson D., Farrah T.,
RA Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA Grabstein K.H., Gliniak B., McAllister I.B., Fanslow W., Alderson M.,
RA Falk B., Gimpel S., Gillis S., Din W.S., Goodwin R.G., Arnitage R.J.;
RA *CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose
RT ligand defines an emerging family of cytokines with homology to
RT TNF.
RL Cell 73:1349-1360(1993).
CC -1- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF
CC T CELLS.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD153 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd153.htm".
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC
CC -----
CC EMBL; L09753; AAA74594.1; -.
CC PIR; A40710; A40710.
CC MIM; 603875;
CC InterPro; IPR003638; TNF_8.
CC InterPro; IPR000478; TNF_family.
CC Pfam; PF00229; TNF; 1.
CC ProDom; PD023087; TNF; 1.
CC SMART; SM00207; TNF; 1.
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DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 62 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 63 234 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 234 AA; 26017 MW; C653615682305B1B CRC64;

Query Match 71.4%; Score 814.5; DB 1; Length 234;
Best Local Similarity 70.6%; Pred. No. 2.7e-67;
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

Qy 1 MQVQGSVASPRSTRPWRSTSRYSFYLSSTALVCLVAVAILLVVQVKDSTPNTTE 59
Db 20 MHVPAGSVAS-----HLGTTSRSYFLTATLALCLVFTVAFIMVLVQVQTSIPNSPD 73

Qy 60 KAPLKGNCSEDLCTLKSTPSKSWAYLVQSKHLNNTKLSWNEGTTHGLIYQDGNLIV 119
Db 74 NVPLKGGNCSEDLCTLKSTPSKSWAYLVQSKHLNNTKLSWNEGTTHGLIYQDGNLIV 133

Qy 120 QPGLFYVCOQLQFLVQCSNHSVDLTQLLINSKIKKOTLVTVCSGVQSKNIYQNLSQL 179
Db 134 QPGLFYVCOQLQFLVQCSNHSVDLTQLLINSKIKKOTLVTVCSGVQSKNIYQNLSQL 193

Qy 180 LHYLVNSTISVRVDFNYVDNTFPDLNLSVFLYSSSD 220
Db 194 LLDYLVNSTISVRVDFNYVDNTFPDLNLSVFLYSSSD 234

RESULT 3
FASL_MOUSE
ID FASL_MOUSE STANDARD; PRT; 279 AA.
AC P41047; Q61217; Q9RIF2;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE FAS ANTIGEN LIGAND.
GN TNFSF6 OR APTLGI OR FASL OR GLD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A. (ISOFORM FASL).
RP MEDLINE=94185175; PubMed=7511063;
RX Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
RA Suda T., Nagata S.;
RT "Generalized lymphoproliferative disease in mice, caused by a point
RT mutation in the Fas ligand.";
RL Cell 76:969-976(1994).
[2]
SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.
RP STRAIN-C57BL/6;
RX MEDLINE=95388076; PubMed=7544870;
RA Peltsch M.J., Tschoep J.J.;
RT "Comparative molecular modelling of the Fas-ligand and other members
RT of the TNF family.";
RL Mol. Immunol. 32:761-772(1995).
[3]
SEQUENCE FROM N.A. (ISOFORM FASL).
RP MEDLINE=95196085; PubMed=7889405;
RX Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a
RT TNF family gene cluster.";
RL Immunity 1:131-136(1994).
[4]
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 22, 2002, 08:30:35 ; Search time 96.97 Seconds
(without alignments)
331.854 Million cell updates/sec

Title: US-09-628-126-19
Perfect score: 1141
Sequence: 1 MQVPGSVASVPRSTRPWS.....DTNTPDLNLSVFLYSSD 220

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : SPTREMBL_17.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phage.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	794.5	69.6	234	043404	Q43404 homo sapien
2	90.5	7.9	797	12 Q99BV2	Q99bv2 human immun
3	89.5	7.8	225	13 Q9IB42	Q9ib42 paralichthy
4	89.5	7.8	401	2 P72902	P72902 synechocyst
5	89.5	7.8	847	12 Q9WIS1	Q9wis1 human immun
6	89	7.8	169	11 Q9WV90	Q9wv90 marmota mon
7	88	7.7	234	6 Q28320	Q28320 capra hircu
8	87	7.6	858	12 Q99C07	Q99c07 human immun
9	87	7.6	896	10 Q9M9B0	Q9m9b0 arabidopsis
10	87	7.6	2013	5 Q96216	Q96216 plasmodium
11	86.5	7.6	2195	6 Q92822	Q92822 saccharomyc
12	86	7.5	280	6 Q9MYL6	Q9myl6 macaca neme
13	86	7.5	280	6 Q9BDN1	Q9bdn1 cercocobus
14	86	7.5	280	6 Q9BDM5	Q9bdm5 macaca mula
15	86	7.5	674	3 Q06629	Q06629 saccharomyc
16	85.5	7.5	994	10 Q9C637	Q9c637 arabidopsis
17	85	7.4	699	12 Q9DP26	Q9dp26 human immun
18	85	7.4	852	12 Q99B27	Q99bz7 human immun
19	84.5	7.4	208	2 Q68241	Q68241 pantoea cit

20	84.5	7.4	217	11 Q9ERG6	Q9erg6 peromyscus
21	84.5	7.4	884	10 Q81069	Q81069 arabidopsis
22	84	7.4	424	11 Q9DC72	Q9dc72 mus musculu
23	84	7.4	1110	10 Q9SDA5	Q9sda5 arabidopsis
24	83	7.3	282	6 Q9BEA8	Q9bea8 sus scrofa
25	82.5	7.2	966	11 Q99K63	Q99k63 mus musculu
26	82	7.2	282	12 Q9IC83	Q9ic83 kaposi's sa
27	81.5	7.1	151	5 Q9GP20	Q9gp20 globodera r
28	81.5	7.1	304	5 Q94382	Q94382 caenorhabdi
29	81.5	7.1	304	5 Q94383	Q94383 caenorhabdi
30	81	7.1	866	10 Q9SUN4	Q9sun4 arabidopsis
31	81	7.1	1391	12 Q9DPR7	Q9dpr7 meleagrid h
32	81	7.1	1409	12 Q9ELH3	Q9elh3 meleagrid h
33	80.5	7.1	216	6 Q9BEC4	Q9bec4 talpa europ
34	80.5	7.1	344	10 Q81781	Q81781 arabidopsis
35	80	7.0	165	1 Q58685	Q58685 methanococc
36	80	7.0	232	4 Q9UIV3	Q9uiv3 homo sapien
37	80	7.0	358	12 Q71050	Q71050 human immun
38	80	7.0	369	2 Q55952	Q55952 synechocyst
39	80	7.0	400	12 Q11578	Q11578 human immun
40	80	7.0	403	12 Q11580	Q11580 human immun
41	79.5	7.0	399	12 Q11584	Q11584 human immun
42	79.5	7.0	889	10 Q9SNA3	Q9sna3 arabidopsis
43	79	6.9	350	4 Q9NSP7	Q9nsp7 homo sapien
44	79	6.9	364	4 Q9HB11	Q9hb11 homo sapien
45	79	6.9	366	2 Q9REN2	Q9ren2 buchnera ap

ALIGNMENTS

RESULT 1
O43404 PRELIMINARY; PRT; 234 AA.
AC O43404;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CD30L PROTEIN.
GN CD30L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98007874; PubMed=9349718;
RA Croager E.J., Abraham L.J.;
RT "Characterisation of the human CD30 ligand gene structure.";
RL Biochim. Biophys. Acta 1353:231-235(1997).
DR EMBL; AF006384; AAB97877.1;
DR EMBL; AF006381; AAB97877.1; JOINED.
DR EMBL; AF006382; AAB97877.1; JOINED.
DR EMBL; AF006383; AAB97877.1; JOINED.
DR InterPro; IPR000478; TNF_family.
DR InterPro; IPR003638; TNF_8.
DR Pfam; PF002229; TNF; 1.
DR PRODOM; PD023087; TNF_8; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
DR SMART; SM00207; TNF; 1.
SQ SEQUENCE 234 AA; 25963 MW; 37BA5733C7911751 CRC64;

Query Match 69.6%; Score 794.5; DB 4; Length 234;
Best Local Similarity 69.2%; Pred. No. 2.3e-68;
Matches 153; Conservative 26; Mismatches 35; Indels 7; Gaps 2;
QY 1 MQVPGSVASVPRSTRPWSRYSFYFYSTAL-VCLVVAVAILLVVQKKDSTPNTTE 59
+ + + + + : + + + + + : + + + + + : + + + + + : + + + + + :
Db 20 MHPVAGSVAS-----HLGTTSRSYFYLTATLALCLVFTVATIMVLVVQRTDSIPNSPD 73
QY 60 KAPLKGNCSEDLFCTLKSTPSKKSWAYLQYSKHLNNTKLSWNEDGTIHGLIYQDGNLIV 119

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Db 74 NVPLKGCNCSDDLCLILKRAFFKSWAYLQVAKHLNKTLSWKNKGDLHGVRYQDGNLVI 133
QY 120 OFFGLYFIVCOLQFLVQCSNHSVDLTQLLLINSIKKQTLVTVCGESGVQSKNIYQNLISQF 179
Db 134 OFFGLYFIIQCLQFLVQCPNNSVDLKKXELLINKHKQXLVTVCGESGMQTKHVYQNLISQF 193
QY 180 LLHYLQVNSTISVRVDFNQVDFNTFFDLNVLVSFLVSSSD 220
Db 194 LLDYLOVNTTISVNDVTQXIDTSTFFPLENVLSIFLXNSD 234

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Q99BY2
ID Q99BY2 PRELIMINARY; PRT; 797 AA.
AC Q99BY2;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Suthent R., Srisurapanon S.;
RT "Biological and immunological characteristics of HIV-1 subtype E in cerebrospinal fluid and blood.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF322200; AAK09407.1; -.
FT NON_TER 1
FT NON_TER 797
SQ SEQUENCE 797 AA; 90476 MW; 1C192A1DE05992C2 CRC64;

Query Match 7.9%; Score 90.5; DB 12; Length 797;
Best Local Similarity 22.5%; Pred. No. 2.2;
Matches 43; Conservative 36; Mismatches 59; Indels 53; Gaps 11;

QY 40 VAILLVVQKDKSTPNTTEKAPLKGNCSEDL-FCTLKST---PSKKSWAY-----LQV 90
Db 72 LCVTLEKTEAKLNKTNTTND-PKIGNLTDEVNRCSFKMTTELKDKKQKVYALFYKLDI 130
QY 91 SKHLNNTKLSWEDGTTHGLIYODGNLIVO-----FPGLYFIV----- 128
Db 131 VPKEKNNSYSE-----YRLNCTSVIKQACPKISFDPIPIHYCTPAGTAYLKCNDKNF 186
QY 129 -----COLQFLVQCSNHSVD--LTQLLLINSIKKQTLVTVCGESGVQSKNIYQNLISQFLL 181
Db 187 NGTGPCKNVSSVQCT-HGKIPVVTQLLNGSLAEIEII-----IRSENLTNNAKNIIV 239
QY 182 HY---LQVNST 189
Db 240 HLKNSVEINCT 250

RESULT 3
Q9IB42
ID Q9IB42 PRELIMINARY; PRT; 225 AA.
AC Q9IB42;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR.
OS Paralicthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidel; Bothidae; Paralicthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
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RA Hirono I., Nam B., Kurobe T., Aoki T.;
RT "Molecular cloning, characterization and expression of tumor necrosis factor (TNF) cDNA and gene from Japanese flounder Paralicthys olivaceus.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB040448; BAA94969.1; -.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNCRSISFCT.
DR SMART; SMO0207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 225 AA; 24965 MW; 8F947FB25FC82658 CRC64;

Query Match 7.8%; Score 89.5; DB 13; Length 225;
Best Local Similarity 25.4%; Pred. No. 0.7;
Matches 31; Conservative 23; Mismatches 57; Indels 11; Gaps 5;

QY 33 LVCLVVAVAILLVVQKDKSTPNTTEKAPLKGNCSE--DLFCTLKSTPSK-KSWAYL- 88
Db 10 IVALCLGGVLAFSWYTNKSEMMTQSGQTAAALSKDKAEKTEPHNTLRQISSRAKAAHLE 69
QY 89 ---QVSKHLNNTKLSW-NEDG---TIHGLIYODGNLIVPGLYFIVCOLQFLVQCSNHS 141
Db 70 GRDEEETSENKLVNKNDEGLAFTQGGPELVNDHIIIPRSGLYFVYSQASFRVSCSDD 129
QY 142 VD 143
Db 130 AD 131

RESULT 4
P72902
ID P72902 PRELIMINARY; PRT; 401 AA.
AC P72902;
DT 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 46.0 KDA PROTEIN.
GN SLR1066.
OS Synecochystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecochystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hiroseawa M., Sugiyura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium Synecochystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL; D90901; BAA16918.1; -.
DR InterPro; IPR001296; Glycos_transf_1.
DR Pfam; PF00534; Glycos_transf_1; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 401 AA; 45951 MW; 9A8C3E0C64933271 CRC64;

Query Match 7.8%; Score 89.5; DB 2; Length 401;
Best Local Similarity 26.6%; Pred. No. 1.3;
Matches 42; Conservative 13; Mismatches 50; Indels 53; Gaps 6;

QY 71 DLFCTLKSTPSKKSWAYL-----QVSKHLN-----NTKLSWNEGDGTH 108
Db 47 DAFPEIKSLPPLKLLWLRLFWPSPSQRAKEYIQKIANFFDIIDAQOGNLPFSKEE----- 101
QY 109 GLIYQDGNLIVQFPGLYFIVCOLQFLVQ-----CSNHSVDLTQLLLINSIKKQTLVTV 162
Db 102 --LAFNGTLIVRSVGLYAFHQFQELVQKTNLSGNVNNVFKLLLRKLRKIKQKQN----- 155
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 22, 2002, 08:22:26 ; Search time 39.95 Seconds
(without alignments)
123.923 Million cell updates/sec

Title: US-09-628-126-19
Perfect score: 1141
Sequence: 1 MQVOPGVSAPWRSTRPWS.....DTNFTPLDNVLVFLYSSD 220

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2.6/ptodata/2/1aa/5A-COMB.pep.*
2: /cgn2.6/ptodata/2/1aa/5B-COMB.pep.*
3: /cgn2.6/ptodata/2/1aa/6A-COMB.pep.*
4: /cgn2.6/ptodata/2/1aa/6B-COMB.pep.*
5: /cgn2.6/ptodata/2/1aa/PCTUS-COMB.pep.*
6: /cgn2.6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	1141	100.0	220	1 US-08-225-989-19	Sequence 19, Appl
2	1141	100.0	220	1 US-08-570-923-19	Sequence 19, Appl
3	1141	100.0	220	1 US-08-580-014-19	Sequence 19, Appl
4	1141	100.0	220	4 US-09-079-785-19	Sequence 19, Appl
5	1141	100.0	239	1 US-08-225-989-6	Sequence 6, Appl
6	1141	100.0	239	1 US-08-570-923-6	Sequence 6, Appl
7	1141	100.0	239	4 US-08-580-014-6	Sequence 6, Appl
8	1141	100.0	239	4 US-09-079-785-6	Sequence 6, Appl
9	814.5	71.4	215	1 US-08-225-989-23	Sequence 23, Appl
10	814.5	71.4	215	1 US-08-570-923-23	Sequence 23, Appl
11	814.5	71.4	215	1 US-08-580-014-23	Sequence 23, Appl
12	814.5	71.4	215	4 US-09-079-785-23	Sequence 23, Appl
13	814.5	71.4	234	1 US-08-225-989-8	Sequence 8, Appl
14	814.5	71.4	234	1 US-08-570-923-8	Sequence 8, Appl
15	814.5	71.4	234	1 US-08-580-014-8	Sequence 8, Appl
16	814.5	71.4	234	4 US-09-079-785-8	Sequence 8, Appl
17	685	60.0	130	1 US-08-225-989-21	Sequence 21, Appl
18	685	60.0	130	1 US-08-570-923-21	Sequence 21, Appl
19	685	60.0	130	1 US-08-580-014-21	Sequence 21, Appl
20	685	60.0	130	4 US-09-079-785-21	Sequence 21, Appl
21	624	54.7	148	3 US-08-584-031-12	Sequence 12, Appl
22	388.5	34.0	125	1 US-08-225-989-20	Sequence 20, Appl
23	388.5	34.0	125	1 US-08-570-923-20	Sequence 20, Appl
24	388.5	34.0	125	1 US-08-580-014-20	Sequence 20, Appl
25	388.5	34.0	125	4 US-09-079-785-20	Sequence 20, Appl
26	229	20.1	52	4 US-09-369-494-17	Sequence 17, Appl
27	229	20.1	52	4 US-09-358-569D-15	Sequence 15, Appl

28 104 9.1 279 5 PCT-US95-00362-5 Sequence 5, Appli
29 88.5 7.8 309 1 US-08-236-918A-2 Sequence 2, Appli
30 85 7.4 291 1 US-08-670-354-6 Sequence 6, Appli
31 85 7.4 291 4 US-09-320-424-6 Sequence 6, Appli
32 85 7.4 291 5 PCT-US96-10895-6 Sequence 6, Appli
33 84 7.4 281 2 US-08-810-453-2 Sequence 2, Appli
34 84 7.4 281 3 US-08-815-190A-2 Sequence 2, Appli
35 84 7.4 281 4 US-09-290-640-25 Sequence 25, Appli
36 84 7.4 281 4 US-09-479-524-3 Sequence 3, Appli
37 84 7.4 281 5 PCT-US95-00362-2 Sequence 2, Appli
38 83.5 7.3 287 3 US-08-815-190A-16 Sequence 16, Appli
39 83 7.3 550 2 US-08-417-210A-140 Sequence 140, App
40 83 7.3 551 2 US-08-417-210A-137 Sequence 137, App
41 83 7.3 551 2 US-08-417-210A-143 Sequence 143, App
42 83 7.3 857 1 US-08-032-835-4 Sequence 4, Appli
43 83 7.3 857 1 US-08-388-809-4 Sequence 4, Appli
44 83 7.3 857 2 US-08-647-714-4 Sequence 4, Appli
45 82.5 7.2 183 4 US-09-105-343A-8 Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-08-225-989-19
; Sequence 19, Application US/08225989
; Patent No. 5480981
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644

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;
;
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-225-989-19

Query Match          100.0%; Score 1141; DB 1; Length 220;
Best Local Similarity 100.0%; Pred. No. 2.3e-110;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQVQGSVSPWRSTRPWRSTRSYFYLSTTALVCLVAVAILLVVQKKDSTPNTTEK 60
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Db 1 MQVQGSVSPWRSTRPWRSTRSYFYLSTTALVCLVAVAILLVVQKKDSTPNTTEK 60
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QY 61 APLKGGNCSEDLFCTLKSTPSKKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQ 120
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Db 61 APLKGGNCSEDLFCTLKSTPSKKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQ 120
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QY 121 FPGLYFVICOLOFLVQCSNHSVDLTQLLINSKIKKOTLVTVCSGVQSKNIYQNLISOFL 180
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Db 121 FPGLYFVICOLOFLVQCSNHSVDLTQLLINSKIKKOTLVTVCSGVQSKNIYQNLISOFL 180
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QY 181 LHYLQVNSTISVRVDFNQYVDNTFFPLDNVLSVFLYSSSD 220
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* RESULT 2
US-08-570-923-19
; Sequence 19, Application US/08570923
; Patent No. 5677430
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,923
; FILING DATE: 12-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
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;
;
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-570-923-19

Query Match          100.0%; Score 1141; DB 1; Length 220;
Best Local Similarity 100.0%; Pred. No. 2.3e-110;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQVQGSVSPWRSTRPWRSTRSYFYLSTTALVCLVAVAILLVVQKKDSTPNTTEK 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MQVQGSVSPWRSTRPWRSTRSYFYLSTTALVCLVAVAILLVVQKKDSTPNTTEK 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 61 APLKGGNCSEDLFCTLKSTPSKKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQ 120
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 APLKGGNCSEDLFCTLKSTPSKKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQ 120
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QY 121 FPGLYFVICOLOFLVQCSNHSVDLTQLLINSKIKKOTLVTVCSGVQSKNIYQNLISOFL 180
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 FPGLYFVICOLOFLVQCSNHSVDLTQLLINSKIKKOTLVTVCSGVQSKNIYQNLISOFL 180
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 181 LHYLQVNSTISVRVDFNQYVDNTFFPLDNVLSVFLYSSSD 220
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Db 181 LHYLQVNSTISVRVDFNQYVDNTFFPLDNVLSVFLYSSSD 220
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RESULT 3
US-08-580-014-19
; Sequence 19, Application US/08580014
; Patent No. 5753203
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,014
; FILING DATE: 20-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 22, 2002, 08:17:46 ; Search time 55.1 Seconds
(without alignments)
297.233 Million cell updates/sec

Title: US-09-628-126-23
Perfect score: 1118
Sequence: 1 MHPAGSVASHLGTTSRSYF.....DTSTFPLENLSIFLYNSD 215
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1118	100.0	234	2 A40710	CD30 ligand - huma
2	814.5	72.9	239	2 B40710	CD30 ligand - mouse
3	112	10.0	279	2 A53062	Fas ligand - mouse
4	96.5	8.6	234	1 JQ1344	tumor necrosis fac
5	94	8.4	235	2 I54490	tumor necrosis fac
6	93.5	8.4	547	2 T30704	rifampicin resista
7	90.5	8.1	281	2 I38707	Fas ligand - human
8	90	8.1	233	1 S22052	tumor necrosis fac
9	89	8.0	809	2 T38051	hypothetical prote
10	87.5	7.8	813	2 T12506	hypothetical prote
11	86	7.7	278	2 A49266	faz ligand - rat
12	85.5	7.6	309	2 I53384	4-1BB ligand - mou
13	85	7.6	235	1 OWMSN	tumor necrosis fac
14	84.5	7.6	232	1 S12606	tumor necrosis fac
15	83.5	7.5	234	1 JH0529	tumor necrosis fac
16	83	7.4	636	2 S70877	hypothetical prote
17	83	7.4	1385	2 T18213	paraspinal crystal
18	82	7.3	1385	2 B96524	hypothetical prote
19	82	7.3	1339	2 G84764	hypothetical prote
20	81.5	7.3	461	2 JN0129	ID-myo-inositol-tr
21	81	7.2	233	1 QWHUN	tumor necrosis fac
22	81	7.2	547	2 H65107	hypothetical 61.6
23	81	7.2	1289	2 T18212	paraspinal crystal
24	80.5	7.2	430	2 T28318	ORF MSV157 hypothe
25	80.5	7.2	434	1 S61999	hypothetical prote
26	80.5	7.2	439	2 A55346	phosphoprotein pho
27	80	7.2	235	2 J00029	tumor necrosis fac
28	79.5	7.1	233	1 S24642	tumor necrosis fac
29	79	7.1	800	2 S53079	PET111 protein - y

30 78.5 7.0 426 2 S64748 mitochondrial oute
31 78.5 7.0 1130 2 T29089 alpha-mannosidase
32 78.5 7.0 1830 2 E82909 conserved hypothet
33 77.5 6.9 492 2 S42735 cytochrome-c oxida
34 77.5 6.9 610 2 S71758 DEAD box protein M
35 77.5 6.9 623 2 B96681 F5I14.14 [imported
36 77 6.9 329 2 T28412 ORF MSV251 hypothe
37 77 6.9 456 2 B96688 unknown protein, 1
38 76.5 6.8 478 2 T27714 hypothetical prote
39 76.5 6.8 619 2 S54636 probable membrane
40 76.5 6.8 3512 2 T17121 CPY protein - midg
41 76 6.8 467 2 D86485 protein F28J9.13 [l
42 76 6.8 479 2 E42508 ELL protein - vacc
43 76 6.8 607 2 E70165 hypothetical prote
44 76 6.8 829 2 S72366 DNA topoisomerase
45 75.5 6.8 284 2 F81431 ABC transporter AT

ALIGNMENTS

RESULT 1
A40710
CD30 ligand - human
C:Species: Homo sapiens (man)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 21-Jul-2000
C:Accession: A40710
R:Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrar, T.; Baker, E.; Sutherland
Alderson, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage,
Cell 73, 1349-1360, 1993
A:Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de
A:Reference number: A40710; MUID:93313964
A:Accession: A40710
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-234 <SMI>
A:Cross-references: GB:O09753; NID:g349277; PIDN:AAA74594.1; PID:g349278
C:Keywords: cytokine receptor; membrane protein; surface antigen

Query Match 100.0%; Score 1118; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 2.4e-98;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MHPAGSVASHLGTTSRSYFYLTATLALCLVFTVATIMLVVQRTDSIPNSPDNVPLKG 60
Db 20 MHPAGSVASHLGTTSRSYFYLTATLALCLVFTVATIMLVVQRTDSIPNSPDNVPLKG 79
Qy 61 GNCSEDLILKRAPFKKSWAYLQVAKHLNKTLSWKNKGILHGVYQDGNLVIQPPGLY 120
Db 80 GNCSEDLILKRAPFKKSWAYLQVAKHLNKTLSWKNKGILHGVYQDGNLVIQPPGLY 139
Qy 121 FIICQLQFLVQCPNNSVDLKLLELLINKHIKQALVTVCESGMQTKHVYONLSQFLLDYIQ 180
Db 140 FIICQLQFLVQCPNNSVDLKLLELLINKHIKQALVTVCESGMQTKHVYONLSQFLLDYIQ 199
Qy 181 VNTTISNVDTFQYIDTSTFPLENLSIFLYNSD 215
Db 200 VNTTISNVDTFQYIDTSTFPLENLSIFLYNSD 234

RESULT 2
B40710
CD30 ligand - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999
C:Accession: B40710
R:Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrar, T.; Baker, E.; Sutherland
Alderson, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage,
Cell 73, 1349-1360, 1993
A:Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de
A:Reference number: A40710; MUID:93313964
A:Accession: B40710

Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	1118	100.0	234	1	TNFB_HUMAN	P32971 homo sapien
2	814.5	72.9	239	1	TNFB_MOUSE	P32972 mus musculu
3	112	10.0	279	1	FASL_MOUSE	P41047 mus musculu
4	96.5	8.6	234	1	TNFA_MOUSE	P29553 equus cabal
5	94	8.4	233	1	TNFA_HACMU	P48094 macaca mula
6	94	8.4	235	1	TNFA_PERLE	P36939 peromyscus
7	92	8.2	233	1	TNFA_MACFA	P79337 macaca fasc
8	90.5	8.1	281	1	FASL_HUMAN	P48023 homo sapien
9	90	8.1	233	1	TNFA_PAPHU	O77510 papio hamad
10	90	8.1	233	1	TNFA_PAPSP	P33620 papio sp. (
11	89	8.0	809	1	FASL_SCHPO	Q10155 schizosacch
12	86	7.7	278	1	FASL_RAT	P36940 rattus norv
13	85.5	7.6	309	1	41BL_MOUSE	P41274 mus musculu
14	85	7.6	233	1	TNFA_CANFA	P51742 canis famul
15	85	7.6	235	1	TNFA_MOUSE	P06804 mus musculu
16	85	7.6	1220	1	CSAC_BACTU	P56955 bacillus th
17	84.5	7.6	232	1	TNFA_PIG	P32563 sus scrofa
18	83.5	7.5	234	1	TNFA_SHEEP	P23383 ovis aries
19	83	7.4	1385	1	C5AA_BACUD	Q45760 bacillus th
20	81.5	7.3	461	1	IP3K_HUMAN	P32677 homo sapien
21	81	7.2	233	1	TNFA_HUMAN	P01375 homo sapien
22	81	7.2	233	1	TNFA_MARMO	O35734 marmota mon
23	81	7.2	541	1	XHBX_ECOLI	P42640 escherichia
24	81	7.2	1289	1	C5AB_BACUD	Q45753 bacillus th
25	80.5	7.2	499	1	PPP5_RAT	P33042 rattus norv
26	80	7.2	229	1	TNFA_CEREL	P51743 cervus elap
27	80	7.2	235	1	TNFA_RAT	P16599 rattus norv
28	79.5	7.1	233	1	TNFA_BOVIN	Q06599 bos taurus
29	79	7.1	800	1	PTII_YEAST	P08468 saccharomyc
30	78.5	7.0	234	1	TNFA_CAVPO	P51435 cavia porce
31	78.5	7.0	426	1	MMMI_YEAST	P41800 saccharomyc
32	77.5	6.9	670	1	DD18_HUMAN	Q9nvp1 homo sapien
33	76	6.8	479	1	PAP1_VACCC	P21079 vaccinia vi

FT	CARBOHYD	153
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FT	CARBOHYD	153
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FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 234 AA; 26017 MW; C653615682305B1B CRC64;

Query Match 100.0%; Score 1118; DB 1; Length 234;
Best Local Similarity 100.0%; Pred. No. 8.2e-98;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHVPAGSVASHLGTTSRSYFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDVPLKG 60
    |||||
DB 20 MHVPAGSVASHLGTTSRSYFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDVPLKG 79
    |||||

QY 61 GNCSEDLCLIKRAPFKKSWAYLOVAKHLNKTLSWNKDGILHGVRQDGNLVIQFPGLY 120
    |||||
DB 80 GNCSEDLCLIKRAPFKKSWAYLOVAKHLNKTLSWNKDGILHGVRQDGNLVIQFPGLY 139
    |||||

QY 121 FIICQLQFLVQCNNVDLKLLELLINKHIKKQALVTVCESGMOTKHVYQNLSQLLDYLO 180
    |||||
DB 140 FIICQLQFLVQCNNVDLKLLELLINKHIKKQALVTVCESGMOTKHVYQNLSQLLDYLO 199
    |||||

QY 181 VNTTISVNDTFQYIDTSTFPLENVLISFLYSNSD 215
    |||||
DB 200 VNTTISVNDTFQYIDTSTFPLENVLISFLYSNSD 234
    |||||

RESULT 2
TNF8_MOUSE
ID TNF8_MOUSE STANDARD; PRT; 239 AA.
AC P32972;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CD30 LIGAND (CD30-L).
GN TNFSF8 OR CD30LG OR CD30L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=F-cell;
RA Smith C.A., Gruess H.-J., Davis T., Anderson D., Farrah T.,
RA Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA Grabstein K.H., Gliniak B., McAlister I.B., Fanslow W., Alderson M.,
RA Falk B., Gimpel S., Gillis S., Din W.S., Goodwin R.G., Armitage R.J.;
RA "CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose
RT ligand defines an emerging family of cytokines with homology to
RT TNF."
RL Cell 73:1349-1360(1993).
CC -!- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF
CC T CELLS.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L09754; AAA74595.1; -
DR PIR; B40710; B40710.
DR MGD; MGI:88328; Tnfsf8.
DR InterPro; IPR0003638; TNF_8.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD023087; TNF; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
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DR PROSITE; PS00049; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT DOMAIN 1 43 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 44 67 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 68 239 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 239 AA; 26519 MW; 29003157DD425159 CRC64;

Query Match 72.9%; Score 814.5; DB 1; Length 239;
Best Local Similarity 70.6%; Pred. No. 2.5e-69;
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

QY 1 MHVPAGSVAS-----HLGTTSSYFYLTATLALCLVFTVATIMVLVQRTDSIPNSPD 54
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DB 20 MHVPAGSVASPMWRSTRPWRSTRSYFYLTAL-VCLVAVAILVLVQKDSPTNTE 78
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QY 55 NVPLKGGNCSEDLCLIKRAPFKKSWAYLOVAKHLNKTLSWNKDGILHGVRQDGNLVI 114
    |||||
DB 79 KAPLKGNCSEDLCLIKRAPFKKSWAYLOVAKHLNKTLSWNKDGILHGVRQDGNLVI 138
    |||||

QY 115 QPGLYFIICQLQFLVQCNNVDLKLLELLINKHIKKQALVTVCESGMOTKHVYQNLSQL 174
    |||||
DB 139 QPGLYFIICQLQFLVQCNNVDLKLLELLINKHIKKQALVTVCESGMOTKHVYQNLSQL 198
    |||||

QY 175 LLDYLQVNTTISVNDTFQYIDTSTFPLENVLISFLYSNSD 215
    |||||
DB 199 LLDYLQVNTTISVNDTFQYIDTSTFPLENVLISFLYSNSD 239
    |||||

RESULT 3
FASL_MOUSE
ID FASL_MOUSE STANDARD; PRT; 279 AA.
AC P41047; O61217; Q9R1F2;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE FAS ANTIGEN LIGAND.
GN TNFSF6 OR APTLIG1 OR FASL OR GLD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=94185175; PubMed=7511063;
RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
RA Suda T., Nagata S.;
RT "Generalized lymphoproliferative disease in mice, caused by a point
RT mutation in the Fas ligand."
RL Cell 76:969-976(1994).
RN [2]
RN SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.
RC STRAIN=C57BL/6;
RX MEDLINE=95388076; PubMed=7544870;
RA Peitsch M.J., Tschoop J.J.;
RT "Comparative molecular modelling of the Fas-ligand and other members
RT of the TNF family."
RL Mol. Immunol. 32:761-772(1995).
RN [3]
RN SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=95196085; PubMed=7889405;
RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a
RT TNF family gene cluster."
RL Immunity 1:131-136(1994).
RN [4]
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ult No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1094	97.9		234	4	O43404	O43404 homo sapien
2	100	8.9		169	11	Q9W90	Q9w90 marmota mon
3	96.5	8.6		215	6	Q9BEE8	Q9bee8 erlinaeus e
4	95.5	8.5		280	6	Q9BDN1	Q9bdn1 cercocebus
5	94.5	8.5		234	6	Q9TTJ3	Q9ttj3 equus cabal
6	93.5	8.4		547	12	Q98269	Q98269 molluscus c
7	93	8.3		217	11	Q9ERG6	Q9erg6 peromyscus
8	92	8.2		280	6	Q9MYL6	Q9myl6 macaca neme
9	92	8.2		280	6	Q9BDM5	Q9bdm5 macaca mulia
10	83.5	8.0		896	10	Q9M9B0	Q9m9b0 arabidopsis
11	88.5	7.9	217	6	Q9BEG1	Q9beg1 bradypus tr	
12	88	7.9	1109	5	Q9GYH7	Q9gyh7 caenorhabdi	
13	87.5	7.8	216	6	Q9BEC4	Q9bec4 talpa europ	
14	87.5	7.8	813	4	Q9Y4N0	Q9y4n0 homo sapien	
15	87.5	7.8	1003	4	Q9P207	Q9p207 homo sapien	
16	85.5	7.6	462	2	Q9CM44	Q9cm44 pasteurella	
17	85	7.6	282	6	Q9BEA8	Q9bea8 steucrella	
18	85	7.6	761	3	Q9UVJ1	Q9uvj1 candida alb	
19	84.5	7.6	232	4	Q9UIV3	Q9uiv3 homo sapien	

Qy	1	MHPAGSVASHLGTTSRSFYFLTATLALCLVFVATIMLWQTDSPNSPDNVLPG	60
Db	20	MHPAGSVASHLGTTSRSFYFLTATLALCLVFVATIMLWQTDSPNSPDNVLPG	79
Qy	61	GNCSDDLCLIKRAPEKXSWAYLOVAHKLNTKISWNKDGILHGVRQDGNLVIQPGIL	12

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Db 80 GNCSEDLCLIKRAPPKSWAYLQVAKHLNKTLSWNGDGLRGVYQDGNLVIOFFGLY 139
Qy 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKIKKQALVTVCESGMQKHYQNLSQFLDLYLQ 180
Db 140 FIICQLQFLVQCPNNSVDLKLXELLINKHKIKKQXLTVCESGMQKHYQNLSQFLDLYLQ 199
Qy 181 VNTTISVNDTFQYIDTSTPLENVLNLSIFLYNSD 215
Db 200 VNTTISVNDTXQYIDTSTPLENVLNLSIFLYNSD 234

RESULT 2
Q9WV90 PRELIMINARY; PRT; 169 AA.
AC Q9WV90;
DT 01-NOV-1999 (T-REMBLrel. 12, Created)
DT 01-NOV-1999 (T-REMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (T-REMBLrel. 17, Last annotation update)
DE FAS LIGAND (FRAGMENT).
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Scurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=HEALTHY LIVER;
RA Hodgson P.D., Grant M.D., Michalak T.I.;
RT "perforin and Fas/Fas ligand-mediated cytotoxicity in acute and
chronic woodchuck viral hepatitis.";
RL Clin. Exp. Immunol. 0:0-0(1999).
DR EMBL; AF152368; AAD38387.1; -.
DR InterPro; IPR000478; TNE family.
DR InterPro; IPR003263; TNF_5.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD008600; TNF_5; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
DR SMART; SM00207; TNF; 1.
FT NON_TER 1 169
FT NON_TER 169 169
SQ SEQUENCE 169 AA; 19274 MW; FDE395B014717B6B CRC64;
```

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Query Match 8.9%; Score 100; DB 11; Length 169;
Best Local Similarity 24.6%; Pred. No. 0.025;
Matches 32; Conservative 23; Mismatches 45; Indels 30; Gaps 5;

Qy 71 LKRAPFKSWAYLQVAKHLNKTLSWNGDGLRGVYQDGNLVIOFFGLYFIICQLQ 127
Db 40 LRRA-----AHLTGKPNRSRSPLEWEDTYGISLSGVKYQKGLLVINDTGLYFVYSKIY 93

Qy 128 FLVQ-CPNNSVDLKLLELLINKH-----IKKQALVTVCESGM-----QTKH 166
Db 94 FRGQSCNNPPLSHKVVYKNSKYPQDLVLMGKMMNYCTTGQMWARSYLGAVNFSTNDH 153

Qy 167 VYQNLQFL 176
Db 154 LYVNVSELSL 163
```

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RESULT 3
Q9BEE8 PRELIMINARY; PRT; 215 AA.
AC Q9BEE8;
DT 01-JUN-2001 (T-REMBLrel. 17, Created)
DT 01-JUN-2001 (T-REMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (T-REMBLrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR PRECURSOR (FRAGMENT).
GN TNFA.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.
OX NCBI_TaxID=9365;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are
their sister group.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286830; CAC28522.1; -.
FT NON_TER 1 215
FT NON_TER 215 215
SQ SEQUENCE 215 AA; 23696 MW; 3E337E7E65F074EA CRC64;
```

```
Query Match 8.6%; Score 96.5; DB 6; Length 215;
Best Local Similarity 23.3%; Pred. No. 0.075;
Matches 47; Conservative 36; Mismatches 76; Indels 43; Gaps 10;

Qy 18 SYFYLTATLALCLVFTVATIMVLVVQRTDSIPNPDNVPKGGNCSEDLILK--RAP 75
Db 28 SFFLVAGATTFLCLLH---FGVIGPQRDE---FPDNIQLNNA-----LAQTLRSSRTQ 74

Qy 76 FKSWAYLQVAKHLNKTLSWNGD-----ILHGVRVQDGNLVIOFFGLYFIICQLQFLVQ 131
Db 75 SDKPVAHV-VASIKSEGLMESEVANALLANGMLTDNLVPLDGLYLYISQVLFKQ 133

Qy 132 -CPNNSVDLKLLELLINKHK-----QALVTVCES-----GMOTKHVYQNLQSF 174
Db 134 GCPSTHV-----FLTHNIKRYAVSYQKDVNLLSAIKSPQSETPEGAERWYEFYILG 187

Qy 175 LLDYLVQVNTTISVNDTFQYID 196
Db 188 GVFOLEKGDRLSAEINLPDILD 209
```

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RESULT 4
Q9BDN1 PRELIMINARY; PRT; 280 AA.
AC Q9BDN1;
DT 01-JUN-2001 (T-REMBLrel. 17, Created)
DT 01-JUN-2001 (T-REMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (T-REMBLrel. 17, Last annotation update)
DE CD95L PROTEIN.
GN CD95L.
OS Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Cercocebus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing and homology analysis of nonhuman primate
Fas/Fas-Ligand and co-stimulatory molecules.";
RL Immunogenetics 0:0-0(2001).
DR EMBL; AF34847; AAK37606.1; -.
SQ SEQUENCE 280 AA; 31407 MW; 729EA60067B7D398 CRC64;
```

```
Query Match 8.5%; Score 95.5; DB 6; Length 280;
Best Local Similarity 27.1%; Pred. No. 0.13;
Matches 35; Conservative 21; Mismatches 46; Indels 27; Gaps 6;

Qy 75 PFKKSW---AYLQVAKHLNKTLSWNGD-GI--LHGVRVQDGNLVIOFFGLYFIICQLQ 128
Db 137 PEKKEQRKVAHLTGKPNRSRSPLEWEDTYGISLVSGVKYKGLLVINVTGLYFVYSKVYF 196

Qy 129 LVQ-CPNNSVDLKLLELLINKH-----IKKQALVTVCESGM-----QTKHV 167
Db 197 RGQSTNLPLSHKVVYMRNSKYPQDLVLMGKMMNYCTTGQMWAHSSYLGAVNLSTDLH 256

Qy 168 YQNLQFL 176
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